

# 赋权图上优化问题的 DNA 计算方法研究

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**摘 要** 对赋权图上经典优化问题的 DNA 计算方法进行探讨,改进原有 DNA 计算模型中的权值编码方法,提出一些新的 DNA 编码方法及 DNA 算法.具体地说,通过设计赋权无向图的相对长度图给出了旅行商问题的一种相对长度 DNA 编码方法及 DNA 算法,通过设计赋权无向图的广义边图给出了中国邮递员问题的一种广义边图 DNA 编码方法及 DNA 算法,通过选取 DNA 序列的最佳逆补比对给出了最小生成树问题的一种基于逆补比对的 DNA 编码方法及 DNA 算法,通过设计从顶点覆盖问题到 Hamilton 回路问题的一种改进多项式变换给出了顶点覆盖问题的一种基于多项式变换的 DNA 编码方法及 DNA 算法.所设计的 DNA 计算方法提高了 DNA 计算中表示数值和处理数值的能力.

**关键词** 智能计算;DNA 计算;算法;优化问题;赋权图  
**中图法分类号** TP301

## Research on DNA Computing Methods of Optimization Problems on Weighted Graph

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**Abstract** This paper discusses DNA computing methods of classical optimization problems on weighted graph. By improving the methods of encoding weights in the previous DNA computing model, this paper proposes some new DNA encoding methods and DNA algorithms for optimization problems. Specifically, by designing the relative length graph of a weighted and undirected graph, it gives a DNA encoding method and DNA algorithm based on relative length graph for the traveling salesman problem; by designing the general line graph of a weighted and undirected graph, gives a DNA encoding method and DNA algorithm based on general line graph for the Chinese postman problem; by selecting the best one of reverse complement alignments of DNA sequences, gives a DNA encoding method and DNA algorithm based on reverse complement alignment for the minimum spanning tree problem; by designing an improved polynomial transformation from the vertex cover problem to the Hamilton circle problem, gives a DNA encoding method and DNA algorithm based on polynomial transformation for the vertex cover problem. The proposed DNA computing methods improve the capability of representing and dealing with data in DNA computing.

**Keywords** intelligent computing; DNA computing; algorithm; optimization problem; weighted graph

### 1 Introduction

DNA computing is a new paradigm of parallel

computation based on the interaction between DNA molecules, which develops theoretical computer science by means of molecular biology tech-

niques. The procedure of DNA computing uses DNA molecules as information storage media, and uses the basic techniques of molecular biology as computational operators for copying, synthesizing, separating, sorting, and concatenating information, which solves science problems based on the complement attribute between the bases of different DNA strands. The procedure can be divided into three phases: encoding, computation (molecular biology experiments), and the abstraction of solutions, where the encoding phase maps the problem we want to solve to a set of DNA molecules that can be used to compute by means of molecular biology techniques. The quality of codes directly affects the speed and efficiency of computation.

Currently, the research on DNA computing has made a great progress in theory or experiment methods. Adleman<sup>[1]</sup> presented a DNA computing model of solving the Hamiltonian path problem in 1994. Lipton<sup>[2]</sup> abstracted a parallel model of molecular computation to solve the 3-SAT problem on the basis of Adleman's experiment in 1995. Ouyang et al<sup>[3]</sup> solved the maximal clique problem in 1997. These previous researches on DNA computing do not need to consider the method of encoding weights in DNA strands. With the development of DNA computing techniques, it can be used to solve increasing optimization problems. Therefore, the method of encoding weights in DNA strand is an important issue toward expanding the capability of DNA computing to solve optimization problems. There exist previous works to represent weights in DNA molecules. Narayanan et al<sup>[4]</sup> presented a method of encoding weights by the lengths of DNA strands. Shin et al<sup>[5]</sup> proposed a method of encoding weights by the number of hydrogen bonds in fixed length DNA strand. Yamamoto et al<sup>[6]</sup> proposed a method of encoding weights by the concentrations of DNA strands. Lee et al<sup>[7]</sup> proposed a method of encoding weights by the melting temperatures of fixed-length DNA strands. These encoding methods successfully solve some instances, but there are certain limitations. So we need to do further research on DNA encoding method.

This paper discusses DNA computing methods for the Chinese postman problem (CPP), the traveling salesman problem (TSP), the minimum spanning tree problem (MST), and the vertex cover problem (VCP). By designing DNA encoding methods for certain optimization problems, it takes

full advantage of different DNA sequences to encode weights. This work improves the capability of representing and dealing with data and expands the extent of solving optimization problems in DNA computing.

## 2 Preliminaries to DNA Computing

DNA (deoxyribonucleic acid) is a kind of polymer that is composed of many monomers (deoxyribonucleotide, briefly nucleotide). There are two modes of connecting DNA monomers to a polymer<sup>[8]</sup>: (1) 5-phosphate group of one nucleotide combines with 3-hydroxyl group of another nucleotide through phosphodiester bond. Thus, DNA monomers can combine with each other to form a DNA strand. (2) The base of one nucleotide attracts the base of another nucleotide through hydrogen bonds based on the principle of Watson-Crick complementary bases. Thus, two DNA strands of reverse complement can combine with each other to form a DNA double-strand.

When DNA monomers combine with each other to form a DNA strand, the combination has certain orientation<sup>[9-10]</sup>. Usually, the DNA strand with 5 free-end being located at the most left end and 3 free-end being located at the most right end is marked with  $5'-X_1X_2\cdots X_n-3'$ , and the DNA strand with 3 free-end being located at the most left end and 5 free-end being located at the most right end is marked with  $3'-X_1X_2\cdots X_n-5'$ , where  $X_i$  denotes the  $i$ th base in DNA strand. When DNA strands combine with each other to form DNA double-strand through hydrogen bonds, the combination is subject to the principle of Watson-Crick complementary bases, that is, A matches T and C matches G. Note that, a DNA double-strand is composed of two anti-parallel strands subject to the principle of Watson-Crick complementary bases.

In order to easily describe the methods, the following representation<sup>[11-12]</sup> is used in this paper:  $5'-X_1X_2\cdots X_n-3'$  is written as  $X_1X_2\cdots X_n$ , and  $3'-X_1X_2\cdots X_n-5'$  is written as  $-X_1X_2\cdots X_n$ . For any DNA strand  $s$ , its reversal  $-s$  is called the reverse strand of  $s$ . Let  $h(s)$  denote the mapping function from each base in  $s$  to its complementary base, that is,  $h(A)=T$ ,  $h(G)=C$ ,  $h(C)=G$ ,  $h(T)=A$ . The DNA strand  $h(s)$  is called the complement strand of  $s$ , and its reversal  $-h(s)$  is called the reverse complement of  $s$ . Any DNA strand  $s$  can combine with its reverse complement  $-h(s)$  to form a DNA double-strand through hydrogen bonds.

3 DNA Computing Method Based on Relative Length Graph for TSP

For a weighted, connected and undirected graph  $G=(V,E)$ ,  $v_i \in V, e_{ij} \in E, 1 \leq i, j \leq n$ , where the weight on edge  $e_{ij}$  is  $w_{ij}$ , the traveling salesman problem (TSP) is to find a circle with minimum sum of weights that starts from a certain vertex, ends at the same vertex, and passes through every other vertices once and only once. For any instance of the traveling salesman problem, if some weights are very small or very large, the previous encoding method<sup>[4]</sup> cannot work well. We devise a new DNA encoding method and DNA algorithm based on relative length graph to deal with it. The method encodes weights by the order numbers of weights instead of weights themselves, so it can directly deal with weights of either real numbers or integers, and the obtained solution is not proportional to the length of DNA strand. This makes it can deal with weights in a very broad range.

3.1 Concepts of Order Number of Weight and Relative Length Graph

**Definition 1.** For a weighted and undirected graph  $G=(V,E)$ ,  $v_i \in V, e_{ij} \in E, 1 \leq i, j \leq n$ , where the weight on edge  $e_{ij}$  is  $w_{ij}$ , all the weights are sorted in an increasing order, and the equal weights are at the same position. Thus, all the weights are divided into  $p$  groups according to their position, which are numbered from 1 to  $p$ , respectively. The number of a weight is called the order number of the weight<sup>[13]</sup>.

**Definition 2.** For a weighted and undirected graph  $G=(V,E)$ ,  $v_i \in V, e_{ij} \in E, 1 \leq i, j \leq n$ , where the weight on edge  $e_{ij}$  is  $w_{ij}$ , we remark  $w_{ij}$  with  $w_{ij,k}$  if the order number of  $w_{ij}$  is  $k$ . For each remarked weight  $w_{ij,k}$ , we add  $k-1$  nodes on edge  $e_{ij}$ . The obtained graph  $G'$  is called the relative length graph of  $G$ <sup>[13]</sup>.

According to the definition of relative length graph, the edge  $e_{ij}$  is divided into  $k$  segments if the order number of  $w_{ij}$  is  $k$ . The bigger the order number, the more the segments of the edge. That is, the number of segments of an edge represents the relative length of the edge. Note that the number of segments isn't directly proportional to the value of weight. Consider the edges with weights 2, 1000, 1002, the numbers of segments are 1, 2, 3, respectively.

3.2 DNA Encoding Method Based on Relative Length Graph

For a weighted and undirected graph  $G=$

$(V,E)$ ,  $v_i \in V, e_{ij} \in E, 1 \leq i, j \leq n$ , where the weight on edge  $e_{ij}$  is  $w_{ij}$ ,  $w_{ij} \geq 0$ , the DNA encoding method based on relative length graph for the traveling salesman problem is given as follows:

- (1) Remark each weight  $w_{ij}$  with  $w_{ij,k}$  according to the order number  $k$  of  $w_{ij}$ .
- (2) For each remarked weight  $w_{ij,k}$ , we add  $k-1$  nodes on edge  $e_{ij}$ . The added nodes are respectively marked with  $v'_{e_{ij},1}, v'_{e_{ij},2}, \dots, v'_{e_{ij},k-1}$ . The obtained graph is marked with  $G'$ .
- (3) For each vertex  $v'_i$  in  $G'$ , use DNA strand  $s_i$  of length  $2c(c \in \mathbb{Z}, c \geq 5)$  to encode it.
- (4) For each edge  $e'_{ij}$  in  $G'$ , use DNA strand  $s_{ij} = -h(s''_i s'_j)$  to encode it, where  $s''_i$  denotes the last half of  $s_i$ ,  $s'_j$  denotes the first half of  $s_j$ ,  $-h(s)$  denotes the reverse complement of  $s$ .

Thus, when the vertex codes and the edge codes are mixed together, they can combine with each other to form DNA double strands based on the principle of Watson-Crick complementary bases. This method of encoding weights in DNA strands is called the Relative Length Method (RLM).

Take the graph  $G$  shown in Fig. 1(a) as an example. All the weights are sorted in an increasing order, that is, 1.2, 2, 2.5, 3, so the order numbers of weights 1.2, 2, 2.5, 3 are 1, 2, 3, 4, respectively. Thus, the weights  $w_{12}, w_{13}, w_{14}, w_{15}, w_{23}, w_{34}, w_{35}, w_{45}$  are remarked with  $w_{12,1}, w_{13,3}, w_{14,4}, w_{15,2}, w_{23,4}, w_{34,1}, w_{35,2}, w_{45,3}$ , respectively. For each remarked weight  $w_{ij,k}$ , we add  $k-1$  nodes on edge  $e_{ij}$ . For example, we add two nodes on  $e_{13}$  since  $w_{13}$  is remarked with  $w_{13,3}$ ; we add one node on  $e_{15}$  since  $w_{15}$  is remarked with  $w_{15,2}$ , and so on. The obtained graph  $G'$  is the relative length graph of  $G$ , as shown in Fig. 1(b).

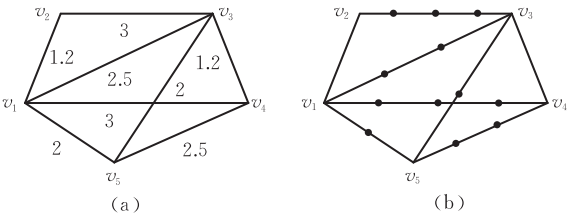


Fig. 1 A weighted graph  $G$  & its relative length graph  $G'$

For each vertex  $v'_i$  in Fig. 1(b), use DNA strand  $s_i$  of length 10 (select  $c=5$ ) to encode it. Here, the added nodes are viewed as vertices. For each edge  $e'_{ij}$  in Fig. 1(b), use DNA strands  $s_{ij} = -h(s''_i s'_j)$  to encode it. Thus, with the help of the property of reverse complementation between the vertex codes and the edge codes, DNA double strands extend continually to form various random

paths including the optimal solution.

### 3.3 DNA Algorithm Based on Relative Length Graph

Given a weighted and undirected graph  $G = (V, E)$ ,  $v_i \in V$ ,  $e_{ij} \in E$ ,  $1 \leq i, j \leq n$ , where the weight on edge  $e_{ij}$  is  $w_{ij}$ ,  $w_{ij} \geq 0$ . Suppose that  $v_1$  is the original vertex just as well. The DNA algorithm based on relative length graph for the traveling salesman problem is given as follows:

(1) Construct the relative length graph  $G' = (V', E')$  of the graph  $G = (V, E)$ .

(2) For the relative length graph  $G'$ , use DNA strand  $s_i$  of length  $2c$  ( $c \in \mathbb{Z}$ ,  $c \geq 5$ ) to encode vertex  $v'_i$ , and use DNA strand  $s_{ij} = -h(s''_i s'_j)$  to encode edge  $e'_{ij}$ .

(3) Merge: DNA strands  $s_i$  and  $s_{ij}$  are mixed together in a single ligation reaction. Based on the principle of Watson-Crick complementary bases, randomly form various DNA double strands.

(4) Denature: DNA double strands are changed into DNA strands by heating.

(5)  $B(N, s_1)$ : Keep all the DNA strands with 5'-end being  $s_1$ , that is, keep all the random paths with the original point being  $v'_1$ .

(6)  $E(N, s_1)$ : Keep all the DNA molecules with 3'-end being  $s_1$ , that is, keep all the random paths with the destination point being  $v'_1$ .

Note that, by the steps (5) and (6), we get all the DNA molecules with 5'-end and 3'-end being  $s_1$ .

(7)  $+(N, s_i)$ : For each vertex  $v'_i$  except  $v'_1$ , keep all the DNA strands with  $s_i$ , that is, keep all the paths with  $v'_i$ .

(8) Separate the shortest path by means of gel electrophoresis.

(9) Sequence the shortest path to determinate its nucleotide sequence, which corresponds to the optimal solution.

### 3.4 Comparison with Previous Methods

Narayanan et al<sup>[4]</sup> proposed a length-based DNA encoding method for the shortest path problem and Han et al<sup>[14]</sup> gave a length-based DNA encoding method for the traveling salesman problem, which encode weights according to the actual length of distance. The relative length method (RLM) is complementary to the previous methods. (1) The previous methods<sup>[4,14]</sup> can only deal with weights of integer, and weights cannot be very small or very large. RLM can deal with weights of either real number or integer, even very small or very large weight. This is because that, in relative length method, the DNA strands used to

encode very large weights are shortened and the DNA strands used to encode very small weights are enlarged. Consider the weights 300, 1, 1000. The order numbers are 2, 1, 3, respectively, so the DNA strands used to encode them are with lengths of 20, 10, 30. (2) In the previous methods, when the difference between the lengths of two paths is very small, such as 100 and 101, gel electrophoresis cannot distinguish them<sup>[4,14]</sup>. This problem can be easily conquered in RLM because with the help of relative length graph, the difference between the lengths of different paths is always above or equal to  $2c$ ,  $c \geq 5$ . (3) In the previous methods, the length of each path is directly proportional to that of DNA strand. Thus, the weights that can be encoded by the previous methods fall in a narrow range. But the solution obtained in RLM isn't proportional to the length of DNA strand, which makes RLM can encode weights in a broad range.

Note that, constructing the relative length graph of a weighted graph needs to add  $\sum_{i=1}^{e-1} i = \frac{e(e-1)}{2}$  nodes in the worst case, where  $e$  denotes the number of edges in the given graph. Compared with the original graph, the scale of the relative length graph increases by  $O(n^2)$ . Therefore, only when there exist very small or very large weights in the given graph or the difference between the lengths of two paths is very small, that is, in the case of the length-based DNA encoding method cannot work well, the relative length method is used to encode weights. So the DNA encoding method based on relative length graph is complementary to the length-based DNA encoding method<sup>[4,14]</sup>.

## 4 DNA Computing Method Based on General Line Graph for CPP

For a weighted, connected and undirected graph  $G = (V, E)$ ,  $v_i \in V$ ,  $e_j \in E$ ,  $1 \leq i \leq n$ ,  $1 \leq j \leq m$ , where the weight on edge  $e_j$  is  $w_j$ , the Chinese postman problem (CPP) is to find a circle with minimum sum of weights that starts from a certain vertex  $v_i$ , ends at  $v_i$ , and passes through each edge at least once. For the Chinese postman problem, this section first proposes the concept of general line graph, and then devises a DNA encoding method and DNA algorithm based on general line edge.

### 4.1 Definition and Construction of General Line Graph

**Definition 3.** For an undirected graph  $G = (V, E)$ ,  $v_i \in V$ ,  $e_j \in E$ ,  $1 \leq i \leq n$ ,  $1 \leq j \leq m$ , a map-

ping function  $f$  is constructed to satisfy: For each edge  $e_j \in E$ , only one vertex  $v'_j$  in  $G'$  satisfies  $f(e_j)=v'_j$ ; for each vertex  $v'_j$  in  $G'$ , only one edge  $e_j$  in  $G$  satisfies  $f^{-1}(v'_j)=e_j$ . If  $e_i$  and  $e_j$  in  $G$  are adjacent, then add an undirected edge between  $v'_i$  and  $v'_j$  in  $G'$ ; if  $v_i$  in  $G$  is an odd degree vertex, then add at most one self-loop to each of the vertices which are mapped from the edges linked to  $v_i$ . The undirected graph obtained by the mapping from edge to vertex is called the general line graph of  $G^{[15]}$ .

Take the weighted and undirected graph  $G$  shown in Fig. 2(a) as an example. The procedure of mapping from edges to vertices is as follows: (1) Map the edges  $e_1, e_2, \dots, e_8$  to the vertices  $v'_1, v'_2, \dots, v'_8$ ; (2) Link the vertices in  $G'$ : Since the edge  $e_1$  is adjacent to  $e_2, e_8, e_7$ , the vertex  $v'_1$  is linked to  $v'_2, v'_8, v'_7$ ; since the edge  $e_2$  is adjacent to  $e_3, e_8, e_1$ , the vertex  $v'_2$  is linked to  $v'_3, v'_8, v'_1$ , and so on. (3) Add the self-loops in  $G'$ : Since  $v_2$  and  $v_6$  are odd degree vertices and the edges linked to  $v_2$  and  $v_6$  are  $e_1, e_2, e_8, e_5, e_6$ , the self-loops are respectively added to  $v'_1, v'_2, v'_8, v'_5, v'_6$ . The constructed general line graph  $G'$  is shown in Fig. 2(b).

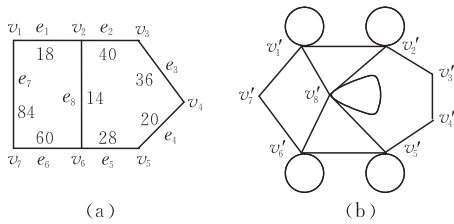


Fig. 2 A weighted and undirected graph  $G$  and its general line graph  $G'$

By means of mapping from edges to vertices, the problem of searching for the shortest circle that passes through each edge at least once is converted into that of searching for the shortest circle that passes through each vertex at least once. Note that the vertex-edge sequence corresponding to the shortest circle isn't only one. For example, the shortest circle in Fig. 2(a) is  $v_1 e_1 v_2 e_2 v_3 e_3 v_4 e_4 v_5 e_5 v_6 e_6 v_7 e_7 v_8 e_8 v_1$  or  $v_1 e_1 v_2 e_8 v_6 e_8 v_2 e_2 v_3 e_3 v_4 e_4 v_5 e_5 v_6 e_6 v_7 e_7 v_1$ , where  $e'_8$  denotes the reversal of  $e_8$ .

4.2 DNA Encoding Method Based on General Line Graph

Given any weighted, connected and undirected graph  $G=(V,E)$ ,  $v_i \in V, e_j \in E, 1 \leq i \leq n, 1 \leq j \leq m$ , where the weight on  $e_j$  is  $w_j, w_j \geq 0, w_j \in \mathbb{Z}^{\text{①}}$ . In order to easily describe the method, suppose that all the weights in graph  $G$  are even. If there exists odd weights, all the weights multiplied by 2. In this case, the obtained optimal solution needs to be

divided by 2. The DNA encoding method based on general line graph for the Chinese postman problem is given as follows:

- (1) Construct the general line graph  $G'$  of the given graph  $G$  by means of mapping from edges to vertices.
- (2) For each vertex  $v'_j$  in  $G'$ , use DNA stand  $s_j$  of length  $w_j$  to encode it, where  $w_j$  is the weight on edge  $e_j$  corresponding to vertex  $v'_j$ .
- (3) For each edge  $e'_{ij}=(v'_i, v'_j)$  in  $G'$ , use DNA strand  $s_{ij}=-h(s''_i s'_j)$  to encode it, where  $s''_i$  denotes the last half of  $s_i, s'_j$  denotes the first half of  $s_j$ , and  $-h(s)$  denotes the reverse complement of  $s$ .

Take the weighted and undirected graph  $G$  shown in Fig. 2(a) as an example. The general line graph  $G'$  is first constructed, as shown in Fig. 2(b). For the vertices  $v'_1, v'_2, \dots, v'_8$  in  $G'$ , select DNA strand  $s_1, s_2, \dots, s_8$  of lengths 18, 40, 36, 20, 28, 60, 84, 14 to encode them, respectively. For each edge  $e'_{ij}=(v'_i, v'_j)$  in  $G'$ , use DNA strand  $s_{ij}=-h(s''_i s'_j)$  to encode it. For example, the code of edge  $e'_{12}=(v'_1, v'_2)$  is  $s_{12}=-h(s''_1 s'_2)$ , whose length is  $18/2+40/2=29$ . Thus, with the help of the property of reverse complementation between the vertex codes and the edge codes, DNA double strands extend continually to form various random paths including the optimal solution.

4.3 DNA Algorithm Based on General Line Graph

Given a weighted, connected and undirected graph  $G=(V,E)$ ,  $v_i \in V, e_j \in E, 1 \leq i \leq n, 1 \leq j \leq m$ , where the weight on  $e_j$  is  $w_j, w_j \geq 0, w_j \in \mathbb{Z}$ . Suppose that  $v'_1$  is the original vertex in the general line graph  $G'$  just as well. DNA algorithm based on general line graph for the Chinese postman problem is given as follows:

- (1) Construct the general line graph  $G'$  of the given graph  $G$  by means of mapping from edges to vertices.
- (2) For each vertex  $v'_j$  in  $G'$ , use DNA stand  $s_j$  of length  $w_j$  to encode it. For each edge  $e'_{ij}=(v'_i, v'_j)$  in  $G'$ , use DNA strand  $s_{ij}=-h(s''_i s'_j)$  to encode it, whose length is  $|w_i|/2+|w_j|/2$ .
- (3) Merge: DNA strands  $s_j$  and  $s_{ij}$  are mixed together in a single ligation reaction. Based on the principle of Watson-Crick complementary bases, randomly form various DNA double strands.
- (4) Denature: DNA double strands are changed into DNA strands by heating.

① If  $w_i$  is a real number, all the weights multiplied by a certain integer (i. e. 10) and then they are rounded into integers.

(5)  $B(N, s_1)$ : Keep all the DNA molecules with 5'-end being  $s_1$ , that is, keep all the random paths with the original point being  $v_1$ .

(6)  $E(N, s_1)$ : Keep all the DNA molecules with 3'-end being  $s_1$ , that is, keep all the random paths with the destination point being  $v_1$ .

(7)  $+(N, s_j)$ : For each vertex  $v'_j$  ( $2 \leq j \leq m$ ) in  $G'$ , keep all the paths with  $v'_j$ .

(8) Separate the shortest path by means of gel electrophoresis.

(9) Sequence the shortest path to determinate its nucleotide sequence, which corresponds to the optimal solution.

#### 4.4 Comparison with Previous Methods

Currently, there exists previous work to encode weights in DNA computing. Narayanan et al<sup>[4]</sup> presented a conceptual encoding method that encodes weights by the lengths of DNA strands. Shin et al<sup>[5]</sup> proposed a method of encoding weights by varying the number of hydrogen bonds in fixed-length DNA strands. Yamamoto et al<sup>[6]</sup> proposed a method of encoding weights by the concentrations of DNA strands. Lee et al<sup>[7]</sup> proposed a method of encoding weights by the melting temperatures of DNA strands. All the above methods are suitable for some specific instances, but the generated random paths in a single ligation reaction are alternant DNA strand and double-strand. The proposed DNA encoding method based on general line graph uses one DNA stand  $s_j$  of length  $w_j$  to encode each vertex  $v'_j$ , and uses one DNA strand  $s_{ij} = -h(s''_i s'_j)$  to encode each edge  $e'_{ij} = (v'_i, v'_j)$ . This makes our method generate DNA double strands instead of alternant DNA strand and double strand in a single ligation reaction. Therefore, the proposed DNA encoding method can generate the optimal solution more easily than the formers, which improves the capability of representing and dealing with data in DNA computing.

### 5 DNA Computing Method Based on Reverse Complement Alignment for MST

For a connected and undirected graph  $G = (V, E)$  with  $n$  vertices, a spanning tree is a subgraph that contains  $n$  vertices and  $n-1$  edges without circle. For a weighted, connected and undirected graph, a minimum spanning tree (MST) is a spanning tree with the minimum weight. The MST problem is to find a minimum spanning tree of the given graph. This section gives a DNA encoding method and DNA algorithm based on reverse complement alignment for the MST problem.

#### 5.1 Definitions of Complement Alignment and Reverse Complement Alignment

Sequence alignment reveals the relations between the characters in different sequences. The alignment  $\alpha$  between sequences  $s$  and  $t$  is the sequence pair  $(s', t')$  which satisfies that<sup>[8]</sup>: (1)  $|s'| = |t'|$ , where  $|x|$  denotes the length of sequence  $x$ ; (2) after deleting all the spaces in  $s'$ , the remaining part is  $s$ ; (3) after deleting all the spaces in  $t'$ , the remaining part is  $t$ ; (4) for each  $i$ ,  $s'[i]$  or  $t'[i]$  is not a space. For any sequence alignment, the relation between two characters is same or different; whereas in DNA double-strand, the relation between two characters is complement, same, or different. So complement alignment and reverse complement alignment of DNA sequences are fitter than sequence alignment in DNA computing.

**Definition 4.** Given an alignment  $\alpha = (s', t')$  between DNA sequences  $s$  and  $t$ . The alignment  $\alpha$  is called a complement alignment<sup>[16]</sup> if  $\alpha$  satisfies: (1) For each  $i$ ,  $s'[i]$  is complementary to  $t'[i]$  if  $s'[i]$  and  $t'[i]$  are not spaces; (2) The orientation of  $s'$  is the same as that of  $t'$ .

**Definition 5.** Given an alignment  $\alpha = (s', t')$  between DNA sequences  $s$  and  $t$ . The alignment  $\alpha$  is called a reverse complement alignment<sup>[16]</sup> if  $\alpha$  satisfies: (1) For each  $i$ ,  $s'[i]$  is complementary to  $t'[i]$  if  $s'[i]$  and  $t'[i]$  are not spaces; (2) The orientation of  $s'$  is opposite to that of  $t'$ .

The method of computing the score of a sequence alignment is as follows<sup>[8]</sup>: For any alignment between two sequences, a bit is assigned to  $+1$  if the two corresponding characters are the same ones (a match); a bit is assigned to  $-1$  if the two corresponding characters are different (a mismatch); a bit is assigned to  $-2$  if one of the two corresponding characters is a space. The sum of the values of all bits in an alignment is called the score of the alignment. The alignment with the biggest score is called the best alignment.

Based on the method of computing the score of sequence alignment, the method of computing the scores of complement alignment and reverse complement alignment is given as follows. For a complement alignment or a reverse complement alignment, a bit is assigned to  $+1$  if the two corresponding characters are complementary (a complement match or a reverse complement match); a bit is assigned to  $-1$  if the two corresponding characters are not complementary (a complement mismatch or a reverse complement mismatch); a bit is assigned to  $-2$  if one of the two corresponding

characters is a space. The sum of the values of all bits in a complement alignment or reverse complement alignment is called the score of the complement alignment or reverse complement alignment. The complement alignment with the biggest score is called the best complement alignment. The reverse complement alignment with the biggest score is called the best reverse complement alignment.

## 5.2 DNA Encoding Method Based on Reverse Complement Alignment for MST

**Definition 6.** For any graph  $G=(V,E)$  with  $n$  vertices, the DNA strand used to distinguish a vertex from other  $n-1$  vertices is called the recognition code of the vertex.

For a weighted, connected and undirected graph  $G=(V,E)$ ,  $v_i \in V, e_{ij} \in E, 1 \leq i, j \leq n$ , where the weight on  $e_{ij}$  is  $w_{ij}$ ,  $w_{ij} \geq 0, w_{ij} \in \mathbb{Z}$ , the length  $l$  of recognition code should satisfy:  $4^{l-1} < n \leq 4^l$ , that is,  $l = \lceil \log_4 n \rceil$ , where 4 is the number of letters in  $\{A, T, G, C\}$ . The DNA encoding method based on reverse complement alignment for the MST problem is given as follows:

(1) Let  $l = \max\{\lceil \log_4 n \rceil, 6\}$ . For each vertex  $v_i$  in  $G$ , use DNA strand  $r_i$  of length  $l$  to encode it. Here, 6 is an empirical value that indicates the minimum length of recognition code.

(2) For each edge  $e_{ij}$  in  $G$ , use DNA strand  $s_{ij}$  of length  $2p = 2 \times \max\{w_{ij}, l\}$  to encode it. Here, the first part of length  $l$  is the same as  $r_i$ , and the last part of length  $l$  is the same as  $r_j$ . And then compute the reverse complement alignment. If  $w_{ij} > l$ , then let  $s_{w_{ij},1}$  denote the first part of length  $w_{ij}$  of  $s_{ij}$ ,  $s_{w_{ij},2}$  denote the last part of length  $w_{ij}$  of  $s_{ij}$ , and compute the reverse complement alignments of  $s_{w_{ij},1}$  and  $s_{w_{ij},2}$ , which are marked with  $\alpha_{s_{w_{ij},1}}$  and  $\alpha_{s_{w_{ij},2}}$ , respectively; otherwise, compute the reverse complement alignments of  $r_i$  and  $r_j$ , which are marked with  $\alpha_{r_i}$  and  $\alpha_{r_j}$ , respectively. Note that, when  $w_{ij}$  is larger than  $l$ ,  $r_i$  or  $r_j$  cannot be the substring of the center part of  $s_{ij}$ .

(3) For any two adjacent edges  $e_{ij}$  and  $e_{jk}$ , add DNA strand  $s_{a_{ij},k}$  as an additional code. Let Upper( $\alpha$ ) denote the upper strand of  $\alpha$ , Lower( $\alpha$ ) denote the lower strand of  $\alpha$ , and “+” denote concatenation. If  $w_{ij} > l$  and  $w_{jk} > l$ , then the additional code  $s_{a_{ij},k} = \text{Lower}(\alpha_{s_{w_{ij},2}}) + \text{Lower}(\alpha_{s_{w_{jk},1}})$ ; if  $w_{ij} \leq l$  and  $w_{jk} \leq l$ , then  $s_{a_{ij},k} = \text{Lower}(\alpha_{r_j}) + \text{Lower}(\alpha_{r_k})$ ; if  $w_{ij} > l$  and  $w_{jk} \leq l$ , then  $s_{a_{ij},k} = \text{Lower}(\alpha_{s_{w_{ij},2}}) + \text{Lower}(\alpha_{r_k})$ ; if  $w_{ij} \leq l$  and  $w_{jk} > l$ , then  $s_{a_{ij},k} = \text{Lower}(\alpha_{r_j}) + \text{Lower}(\alpha_{s_{w_{jk},1}})$ . Thus, DNA strands  $s_{ij}$  and  $s_{jk}$  can combine with  $s_{a_{ij},k}$  to

form DNA double strands, as shown in Fig. 3. Note that, for edges  $e_{ij}$  and  $e_{ji}$ , also add one DNA strand  $s_{a_{ij},i}$  as an additional code.

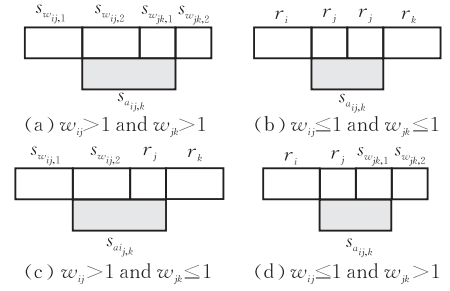


Fig. 3 Joint of DNA strands  $s_{ij}$ ,  $s_{jk}$  and  $s_{a_{ij},k}$

Take the weighted graph  $G$  shown in Fig. 4 as an example. There are 8 vertices and 12 edges in it, so  $l = \max\{\lceil \log_4 8 \rceil, 6\} = 6$ . For each vertex in  $G$ , use a DNA strand of length 6 to encode it. For each edge  $e_{ij}$  in  $G$ , if  $w_{ij} \leq 6$ , DNA strand  $s_{ij}$  is with length of 12, where the first half of  $s_{ij}$  is  $r_i$  and the last half of  $s_{ij}$  is  $r_j$ . If  $w_{ij} > 6$ , DNA strand  $s_{ij}$  is with length of  $2w_{ij}$ , where the first part of length 6 is the same as  $r_i$ , the last part of length 6 is the same as  $r_j$ , and the center part of  $s_{ij}$  is randomly selected but it must exclude  $r_i$  or  $r_j$ . And then compute the reverse complement alignments: If  $w_{ij} \leq 6$ , then compute  $\alpha_{r_i}$  and  $\alpha_{r_j}$ ; otherwise, compute  $\alpha_{s_{w_{ij},1}}$  and  $\alpha_{s_{w_{ij},2}}$ . For the edge  $e_{23}$ , compute  $\alpha_{r_2}$  and  $\alpha_{r_3}$  since  $w_{23} \leq 6$ ; for the edge  $e_{12}$ , compute  $\alpha_{s_{w_{12},1}}$  and  $\alpha_{s_{w_{12},2}}$  since  $w_{12} > 6$ , and so on. For any two adjacent edges  $e_{ij}$  and  $e_{jk}$ , add one DNA strand  $s_{a_{ij},k}$  as an additional code. Consider the edges  $e_{12}$  and  $e_{23}$ , the additional code  $s_{a_{12},3} = \text{Lower}(\alpha_{s_{w_{12},2}}) + \text{Lower}(\alpha_{r_3})$  since  $w_{12} > 6$  and  $w_{23} \leq 6$ .

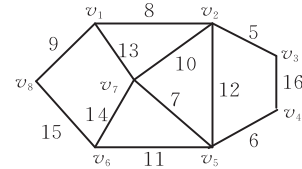


Fig. 4 A weighted and undirected graph  $G=(V,E)$

## 5.3 DNA Algorithm Based on Reverse Complement Alignment

For a weighted, connected and undirected graph  $G=(V,E)$ ,  $v_i \in V, e_{ij} \in E, 1 \leq i, j \leq n$ , where the weight on edge  $e_{ij}$  is  $w_{ij}$ , the DNA algorithm based on reverse complement alignment for the MST problem is given as follows:

(1) Let  $l = \max\{\lceil \log_4 n \rceil, 6\}$ . For each vertex  $v_i$  in  $G$ , use DNA strand  $r_i$  of length  $l$  to encode it.

(2) For each edge  $e_{ij}$  in  $G$ , use DNA strands



$s_{ij}$  of length  $2p = 2 \times \max\{w_{ij}, l\}$  to encode it, where the first part of length  $l$  is the same as  $r_i$ , and the last part of length  $l$  is the same as  $r_j$ . If  $w_{ij} \leq l$ , then compute the reverse complement alignments  $\alpha_{r_i}$  and  $\alpha_{r_j}$ ; otherwise, compute the reverse complement alignments  $\alpha_{s_{w_{ij},1}}$  and  $\alpha_{s_{w_{ij},2}}$ .

(3) For any two adjacent edges  $e_{ij}$  and  $e_{jk}$ , use DNA strand  $s_{a_{ij,k}} = \text{Lower}(\alpha_{s_{w_{ij},2}} | \alpha_{r_j}) + \text{Lower}(\alpha_{s_{w_{jk},1}} | \alpha_{r_j})$  as an additional code, where ' $a|b$ ' denotes either  $a$  or  $b$ . If  $w_{ij} > l$ , then select  $\alpha_{s_{w_{ij},2}}$ , otherwise select  $\alpha_{r_j}$ ; if  $w_{jk} > l$ , then select  $\alpha_{s_{w_{jk},1}}$ , otherwise select  $\alpha_{r_j}$ .

(4) Merge: DNA strands  $s_{ij}$  and  $s_{a_{ij,k}}$  are mixed together in a single ligation reaction. Based on the principle of Watson-Crick complementary bases, randomly form various DNA double strands.

(5) Denature: DNA double strands are changed into DNA strands by heating.

(6)  $-(N, s_{a_{ij,k}})$ : discard all the DNA strands with additional codes. Note that, all the upper strands in the DNA encoding method do exclude additional codes.

(7)  $+(N, r_i)$ : For each vertex  $v_i (1 \leq i \leq n)$ , keep all the DNA strands with recognition code  $r_i$ .

(8) Separate the DNA strands with the minimum weight through gel electrophoresis.

(9) Determine the nucleotide sequence of the DNA strand with the minimum weight. The sequence corresponds to an Euler cycle of the graph, and a MST can be obtained from the Euler cycle.

## 6 DNA Computing Method Based on Polynomial Transformation for VCP

For an undirected graph  $G=(V, E)$  and a positive integer  $p$ , a vertex subset  $V' \subseteq V$  is called a vertex cover if each edge in  $E$  is incident to at least one vertex in  $V'$ . The vertex cover problem (VCP) is to find a vertex cover  $V'$  of size  $p$  in an undirected graph  $G$ . This section presents a hybrid-based DNA solution to the vertex cover problem through designing an improved polynomial transformation from the vertex cover problem to the Hamiltonian circle problem (HCP).

### 6.1 Concepts of Improved Cover Subgraph and Selection Vertex

**Definition 7.** For any edge  $e_j = (v_i, v_k)$  in an undirected graph  $G=(V, E)$ , a newly constructed subgraph shown in Fig. 5 is called the improved cover subgraph of  $e_j$ <sup>[17]</sup>.

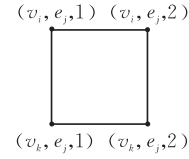


Fig. 5 The improved cover subgraph of edge  $e_j = (v_i, v_k)$

The improved cover subgraph of edge  $e_j = (v_i, v_k)$  has 4 vertices and 4 edges. Each vertex in it is marked with  $(v_i, e_j, x)$  or  $(v_k, e_j, x)$ ,  $1 \leq x \leq 2$ . The set of vertices in the improved cover subgraph of  $e_j$  is marked with  $V_{e_j} = \{(v_i, e_j, 1), (v_i, e_j, 2), (v_k, e_j, 1), (v_k, e_j, 2)\}$ , and the set of edges in it is marked with  $E_{e_j} = \{\langle (v_i, e_j, 1), (v_i, e_j, 2) \rangle, \langle (v_k, e_j, 1), (v_k, e_j, 2) \rangle, \langle (v_i, e_j, 1), (v_k, e_j, 1) \rangle, \langle (v_i, e_j, 2), (v_k, e_j, 2) \rangle\}$ .

**Definition 8.** For an undirected graph  $G=(V, E)$  and a positive integer  $p$ , the vertices in a subset  $V'$  of size  $p$  are called the selection vertices<sup>[18]</sup> if the subset  $V'$  is a vertex cover.

### 6.2 Polynomial Transformation from VCP to HCP

For an undirected graph  $G=(V, E)$ ,  $v_i \in V$ ,  $e_j \in E$ ,  $1 \leq i \leq n$ ,  $1 \leq j \leq m$ , and a positive integer  $p$ , the polynomial transformation from the vertex cover problem to the Hamiltonian circle problem is devised as follows.

(1) Construct the improved cover subgraphs: For each edge  $e_j = (v_i, v_k)$ , the improved cover subgraph of  $e_j$  is constructed, as shown in Fig. 5.

(2) Link the improved cover subgraphs of edges in  $G$  to form  $|V|$  subpaths: Let  $\deg(v_i)$  denote the degree of vertex  $v_i$ , and  $e_{v_i[1]}, e_{v_i[2]}, \dots, e_{v_i[\deg(v_i)]}$  denote the edges incident to  $v_i$ . The improved cover subgraphs of  $e_{v_i[1]}, e_{v_i[2]}, \dots, e_{v_i[\deg(v_i)]}$  are linked by edge set  $E_{v_i} = \{\langle (v_i, e_{v_i[j]}, 2), (v_i, e_{v_i[j+1]}, 1) \rangle \mid 1 \leq j < \deg(v_i) \}$  to form one subpath, as shown in Fig. 6. For any undirected graph  $G=(V, E)$ , the number of subpaths is  $|V|$ , which include all the improved cover subgraphs.

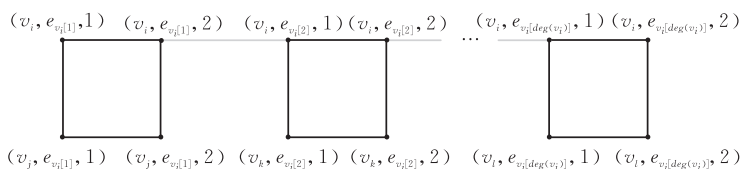


Fig. 6 The connections between the improved cover subgraphs of the edges incident to  $v_i$



(3) Link  $p$  selection vertices to all the subpaths: Let  $a_1, a_2, \dots, a_p$  denote  $p$  selection vertices. Link each selection vertex  $a_j$  to the start point  $(v_i, e_{v_i[1]}, 1)$  and the end point  $(v_i, e_{v_i[\deg(v_i)]}, 2)$  of each subpath by edge set  $E_{a_j} = \{ \langle a_j, (v_i, e_{v_i[1]}, 1) \rangle, \langle a_j, (v_i, e_{v_i[\deg(v_i)]}, 2) \rangle \mid 1 \leq j \leq p, 1 \leq i \leq n \}$ . The obtained graph is marked with  $G' = (V', E')$ , where  $V' = \{ \bigcup_{e_i \in E} V_{e_i} \} \cup \{ \bigcup_{j=1 \sim p} \{a_j\} \}$ ,  $E' = \{ \bigcup_{e_i \in E} E_{e_i} \} \cup \{ \bigcup_{v_i \in V} E_{v_i} \} \cup \{ \bigcup_{j=1 \sim p} E_{a_j} \}$ .

For an undirected graph  $G = (V, E)$  with  $n$  vertices and an integer  $p \leq n$ , the time complexity of the above transformation is analyzed as follows:  $|E| \leq n(n-1)/2 = O(n^2)$ ,  $|V'| = p + 4|E| \leq p + 4n(n-1)/2 = O(n^2)$ ,  $|E'| = 4|E| + \sum_{v_i \in V} (\deg(v_i) - 1) + 2p|V| = 4|E| + (2|E| - |V|) + 2p|V| = 6|E| + (2p-1)|V| = O(n^2)$ . So the transformation can be completed in a polynomial time.

Take the graph  $G = (V, E)$  shown in Fig. 7 and the positive integer  $p=2$  as an example. The improved cover subgraphs of  $e_1, e_2, e_3, e_4, e_5$  are first constructed, and then they are linked by edge set  $E_{v_i} = \{ \langle (v_i, e_{v_i[j]}, 2), (v_i, e_{v_i[j+1]}, 1) \rangle \mid 1 \leq j < \deg(v_i) \}$  to form 4 subpaths. For vertex  $v_1$ , the improved cover subgraphs of  $e_1, e_3, e_4$  are linked together to form one subpath by edges  $\langle (v_1, e_1, 2), (v_1, e_3, 1) \rangle$  and  $\langle (v_1, e_3, 2), (v_1, e_4, 1) \rangle$ ; for vertex  $v_2$ , the improved cover subgraphs of  $e_1$  and  $e_2$  are linked together to form one subpath by edge  $\langle (v_2, e_1, 2), (v_2, e_2, 1) \rangle$ , and so on. And then, all the subpaths are linked with selection vertices by edges  $E_{a_j} = \{ \langle a_j, (v_i, e_{v_i[1]}, 1) \rangle, \langle a_j, (v_i, e_{v_i[\deg(v_i)]}, 2) \rangle \mid 1 \leq j \leq p, 1 \leq i \leq n \}$ , that is,  $\{ \langle a_1, (v_1, e_1, 1) \rangle, \langle a_1, (v_1, e_4, 2) \rangle, \langle a_1, (v_2, e_1, 1) \rangle, \langle a_1, (v_2, e_2, 2) \rangle, \dots, \langle a_2, (v_4, e_4, 1) \rangle, \langle a_2, (v_4, e_5, 1) \rangle \}$ . The obtained graph  $G' = (V', E')$  is shown in Fig. 8.

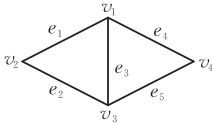


Fig. 7 A weighted and undirected graph  $G=(V, E)$

It can be proved that for any undirected graph  $G=(V, E)$  and a positive integer  $p$ , the graph  $G$  has a vertex cover  $V'$  of size  $p$  if and only if  $G'=(V', E')$  obtained from the improved polynomial transformation has a Hamiltonian circle, where  $V' = \{ \bigcup_{e_i \in E} V_{e_i} \} \cup \{ \bigcup_{j=1 \sim p} \{a_j\} \}$ ,  $E' = \{ \bigcup_{e_i \in E} E_{e_i} \} \cup \{ \bigcup_{v_i \in V} E_{v_i} \} \cup \{ \bigcup_{j=1 \sim p} E_{a_j} \}$ . For the details, please see the reference [18].

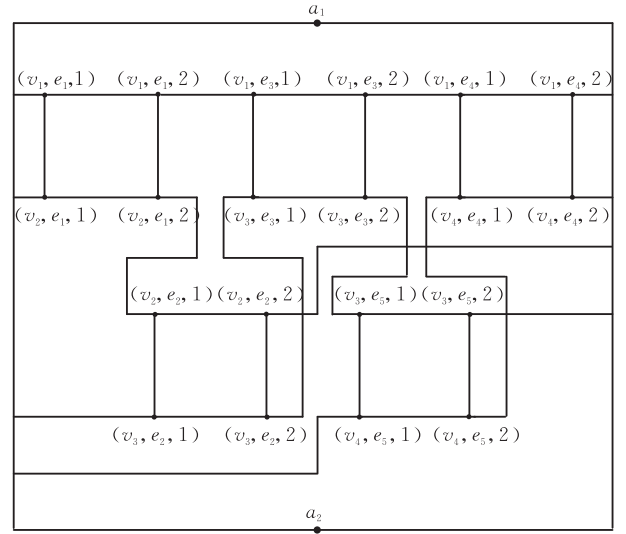


Fig. 8 The connections between the improved cover subgraphs of the edges in graph  $G$

### 6.3 DNA Encoding Method Based on Polynomial Transformation

For an undirected graph  $G=(V, E)$  and a positive integer  $p$ , the DNA encoding method based on the improved polynomial transformation for the vertex cover problem is given as follows:

(1) For each edge  $e_j=(v_i, v_k)$  in  $G$ , construct the improved cover subgraph of  $e_j$ . For all the edges incident to  $v_i$ , the improved cover subgraphs are linked together to form one subpath by edge set  $E_{v_i} = \{ \langle (v_i, e_{v_i[j]}, 2), (v_i, e_{v_i[j+1]}, 1) \rangle \mid 1 \leq j < \deg(v_i) \}$ . The number of the subpaths is  $|V|$ , which include all the improved cover subgraphs of the edges in  $G$ . Link  $p$  selection vertices to the start and end points of each subpath by edge set  $E_{a_j} = \{ \langle a_j, (v_i, e_{v_i[1]}, 1) \rangle, \langle a_j, (v_i, e_{v_i[\deg(v_i)]}, 2) \rangle \mid 1 \leq j \leq p, 1 \leq i \leq n \}$ . The obtained graph is marked with  $G'=(V', E')$ , where  $V' = \{ \bigcup_{e_i \in E} V_{e_i} \} \cup \{ \bigcup_{j=1 \sim p} \{a_j\} \}$ ,  $E' = \{ \bigcup_{e_i \in E} E_{e_i} \} \cup \{ \bigcup_{v_i \in V} E_{v_i} \} \cup \{ \bigcup_{j=1 \sim p} E_{a_j} \}$ .

(2) For each vertex  $v_i$  in  $G'$ , use DNA stand  $s_i$  of length  $l$  to encode it. Here, select  $l=20$ .

(3) For each edge  $e_j=(v_i, v_k)$  in  $G'$ , use the DNA strands  $s_{ik} = -h(s_i''s_k')$  to encode it.

### 6.4 DNA Algorithm Based on Polynomial Transformation

For an undirected graph  $G=(V, E)$  and a positive integer  $p$ , the DNA algorithm based on the polynomial transformation for the vertex cover problem is given as follows.

(1) Convert  $G=(V, E)$  to  $G'=(V', E')$  through the improved polynomial transformation, where  $V' = \{ \bigcup_{e_i \in E} V_{e_i} \} \cup \{ \bigcup_{j=1 \sim p} \{a_j\} \}$ ,  $E' = \{ \bigcup_{e_i \in E} E_{e_i} \} \cup$

$\{\bigcup_{v_i \in V} E_{v_i}\} \cup \{\bigcup_{j=1 \sim p} E_{a_j}\}$ . For each vertex  $v_i$  in  $G'$ , use DNA strand  $s_i$  of length  $l=20$  to encode it. For each edge  $e_j = (v_i, v_k)$  in  $G'$ , use the DNA strand  $s_{ik} = -h(s_i''s_k')$  to encode it.

(2) Merge: DNA strands  $s_i$  and  $s_{ij}$  are mixed together in a single ligation reaction. Based on the principle of Watson-Crick complementary bases, randomly form various DNA double strands.

(3) Denature: DNA double strands are changed into DNA strands by heating.

(4)  $(N, \leq 20 \times n')$ : keep all the DNA molecules whose length are less than or equal to  $20 \times n'$ , where  $n'$  is the number of vertices in  $G'$ .

(5)  $+(N, s_i)$ : For each vertex  $v_i$  in  $G'$ , keep all the DNA molecules with  $s_i$ .

(6) Detect: If any DNA molecule remains, say "Yes"; otherwise say "No". If the answer is "Yes", then separate the DNA molecules obtained in step 5 through agarose gel electrophoresis, and the furthest DNA molecules are just what we want. Sequencing the furthest DNA molecule to determinate its nucleotide sequence, which corresponds to the optimal solution.

## 6.5 Comparison with Previous Methods

For any instance of the vertex cover problem, the previous DNA algorithms<sup>[19-20]</sup> are based on sticker model, and the proposed DNA algorithm is based on hybrid system. Firstly, a polynomial transformation is devised to convert any instance of the vertex cover problem to that of the Hamiltonian circle problem. And then give a DNA encoding method and DNA algorithm based on hybridization for the vertex cover problem. The operations used in the method are implemented more easily than that in the previous methods. Compared with the previous polynomial transformation<sup>[18]</sup>, the improved cover subgraph has 4 vertices and 4 edges instead of 12 vertices and 14 edges. Thus, the number of vertices in the obtained graph  $G'$  is reduced to  $p+4|E|$  from  $p+12|E|$ , and the number of edges is reduced to  $6|E|+(2p-1)|V|$  from  $16|E|+(2p-1)|V|$ .

## 7 Conclusion

This paper discusses DNA computing methods of optimization problems on weighted graph. The proposed DNA encoding method based on relative length graph for the traveling salesman problem can directly deal with weights of real numbers and integers, and can distinguish the paths with almost equal weights. The obtained solution is not pro-

portional to the length of DNA strand, so it can encode weights of broad range. The designed DNA encoding method based on general line graph for the Chinese postman problem uses two DNA stands of different lengths to encode each vertex. This makes the codes of weights on edges are dealt with by the method similar to the codes of vertices, so the weights on edges are dealt with more easily than in the formers. The presented DNA encoding method based on reverse complement alignment for the minimum spanning tree problem selects the additional codes by computing the reverse complement alignment of the first and last parts of edge codes, and finds the minimum spanning tree by getting an Euler circle of the given instance. The proposed DNA encoding method based on polynomial transformation for the vertex cover problem is an improvement on the previous method. The number of vertices and edges in the improved cover subgraph is decreased, and so the space complexity is reduced.

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