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Research Article

Spatial Cluster Analysis by the Adleman-Lipton DNA Computing Model and Flexible Grids

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Spatial cluster analysis is an important data-mining task. Typical techniques include CLARANS, density- and gravity-based clustering, and other algorithms based on traditional von Neumann's computing architecture. The purpose of this paper is to propose a technique for spatial cluster analysis based on DNA computing and a grid technique. We will adopt the Adleman-Lipton model and then design a flexible grid algorithm. Examples are given to show the effect of the algorithm. The new clustering technique provides an alternative for traditional cluster analysis.

1. Introduction

Deoxyribonucleic acid computing, or DNA computing in short, has attracted strong interests and wide focus recently. It is inspired by the similarity between the way DNA stores and manipulates information with traditional Turing machine. Although DNA computing is in a sense similar to evolutionary computing, but the significant difference between them lies in the computing medium, biomolecules rather than transistor chips. It is this difference that makes DNA computing a promising field with ultimate goal of making DNA computers [1].

The essential work to reveal the ability of DNA in computing is by Adleman's experiment (Adleman [2]), which demonstrated that the tools of laboratory molecular biology could be used to solve computation problems. Adleman also proves the huge information storage capacity of DNA which is contained in the sequence of nucleotide bases that hydrogen bonds in a complementary fashion to form double-stranded molecules from single-stranded oligonucleotides. Adleman's work was later generalized by Lipton [3] to the satisfiability problem. Based on Adleman and Lipton's research, a number of applications of DNA computing in solving combinatorially complex problems such as factorization, graph theory, control, and nanostructures have emerged [1]. There appeared also theoretical studies

including DNA computers which are programmable, autonomous computing machines with hardware in biological molecules mode, see [4–7] for references.

Adleman and Lipton's original works include a basic computing model, often referred to as the Adleman-Lipton model. Later generalizations include the sticker model, the splicing model, and the insertion deletion model [1]. However, most applications in this area are restricted to problems of combinatory types due to searching nature of DNA computing. It is a challenge how to design applications of optimization types.

Spatial cluster analysis is a traditional problem in knowledge discovery from databases [8]. It has wide applications since increasingly large amounts of data obtained from satellite images, X-ray crystallography, or other automatic equipment are stored in spatial databases. The most classical spatial clustering technique is due to Ng and Han [9] who developed a variant PAM algorithm called CLARANS, while new techniques are proposed continuously in the literature aiming to reduce the time complexity, or to fit for more complicated cluster shapes.

For example, Bouguila [10] proposed some model-based methods for unsupervised discrete feature selection. Wang et al. [11] developed techniques to detect clusters with irregular boundaries by a minimum spanning tree-based clustering algorithms. By using an efficient implementation of the cut and the cycle property of the minimum spanning trees, they obtain a performance better than $O(N^2)$. In another paper, Wang and Huang [12] developed a new density-based clustering framework by a level set approach. By a valley seeking method data points are grouped into corresponding clusters.

Although DNA computing and cluster analysis receive much attention and rapid development, there have appeared rare combination of these two important research areas. Up to the authors knowledge, the combination of DNA computing and cluster analysis is found in a few researches such as Bakar et al. [7].

Inspired by the research of Bakar et al. [7], this paper focuses on the joint study of DNA computing with cluster analysis. We propose a new grid-based clustering technique which can be solved by DNA computing. Different with other researches, this can reduce the searching space significantly. Finally we present two examples to show the details of our technique.

2. DNA Computing and Operations

2.1. DNA Structures

Macromolecules of nucleic acids are composed of nucleotide building blocks. In DNA, the nucleotides are the purines adenine (A), guanine (G), the pyrimidines thymine (T), and cytosine (C). Single-stranded DNA molecules, or oligonucleotides, are formed by connecting the nucleotides together with phosphodiester bonds. The single strands of DNA can form a double-stranded molecule when the nucleotides hydrogen bonds to their Watson-Crick complements, $\overline{A} = T$ and $\overline{G} = C$ (Figure 1).

DNA stores information in nucleic acid and manipulates information via enzymes and interactions. A strand of DNA is encoded with four bases represented by the letters A, T, C, and G. Each strand has a 3′- and a 5′-end, and hence any single strand has a natural orientation. The cutting of certain strands of a DNA molecule is performed by the restriction enzymes. These enzymes catalyse the cutting operations at very specific DNA base sequences which are called recognition sites. Figure 2(a) shows a DNA molecule in which its four

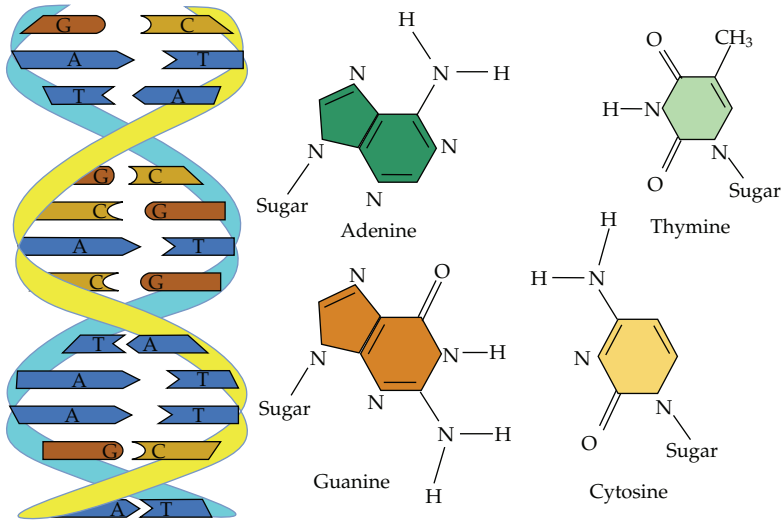


Figure 1: A double-stranded DNA structure diagram.

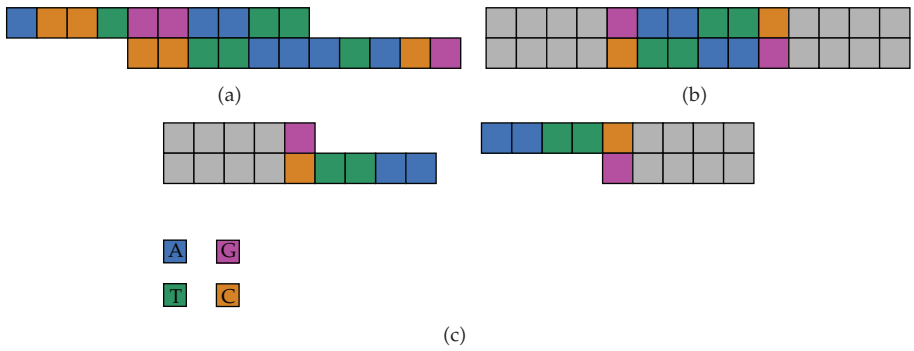


Figure 2: DNA molecules with sticky ends.

nucleotides in the left end and five in the right end are not paired with nucleotides from the opposite strand caused by cutting, or some other operations. In this case, the molecule is called to have sticky ends.

Here is an example which illustrates the process by the enzyme EcoRI as shown in Figure 2(b) where N represents some other arbitrary deoxyribonucleotide. EcoRI acts only at the six-term sequences which are exactly like the form

$$\begin{array}{c} G\ A\ A\ T\ T\ C \\ C\ T\ T\ A\ A\ G. \end{array} \tag{2.1}$$

The effect is to cut the molecule into two pieces as shown in Figure 2(c).

There are over 100 different restriction enzymes, each of which cuts at its specific recognition site. A restriction enzyme cuts DNA into pieces with sticky ends. On the other hand, sticky ends will match and attach to other sticky ends of any other DNA that has been

cut with the same enzyme. DNA ligase joins the matching sticky ends of the DNA pieces from different sources that have been cut by the same restriction enzyme.

2.2. DNA-Computing Models

There are several types of DNA-computing models among which the Adleman-Lipton model is the most traditional one. This model focuses on the hybridization between different DNA molecules as a basic step of computations. According to Adleman and Lipton's original works [2, 3], this traditional DNA-computing strategy is based on enumerating all candidate solutions, and then using some selection process to choose the correct DNA. This technique requires that the size of the initial data pool increases exponentially with the number of variables in the calculation.

Apart from the Adleman-Lipton model, other DNA computing models appeared such as the sticker model, the splicing model. The Sticker model is based on a coding scheme called DNA complex. A DNA complex is a partially double DNA strand. Usually a double piece represents a bit with value one while a single-strand represents zero. Hence each complex is constructed by two single stranded DNA molecules referred to as memory strands and sticker strands. A memory strand contains n nonoverlapping substrands each of which is m bases long. Each sticker strand is m bases long and is complementary to exactly one of the n substrands in a memory strand.

The second model is the splicing model proposed by Tom [6] based on formal language theory. A splicing system $S = (A, L, B, C)$ consists of a finite alphabet A, a finite set I of initial strings in A^* (language over A), and finite sets B and C of triples (c, x, d) with $c, d, x \in A^*$. Each such triple in B or C is called a pattern. For each such triple the string cxd is called a site, and the string x is called a crossing. Patterns in B are called left patterns, and patterns in C are called right patterns. The language $L = L(S)$ generated by S consists of the strings in I and all strings that can be obtained by adjoining to $Lucxfq$ and $pexdv$ whenever $ucsdv$ and $pexfq$ are in L and (c, x, d) and (e, x, f) are patterns of the same hand. A language L is a splicing language if there exists a splicing system S for which $L = L(S)$.

The next model is the k-armed model which is based on some more complicated molecule structures which have three-dimensional DNA architecture. In [13] the authors pointed out that it is natural to use the armed model to represent SAT problem in terms of contact network framework, and they gave theoretical solutions to this NP-complete problems. Like the splicing model, biological operations in the k-armed model include cleaving and connecting.

2.3. Operations of the Adleman-Lipton Model

The basic principle of DNA computing is to use the encoded information in the sequence of nucleotides and evolve them by breaking and making new bonds between them to reach the answer. The basic operations performed by enzymes are denaturing, replicating, merging, detecting, and so forth.

According to the DNA computing models proposed by Adleman [2] and Lipton [3], there are several basic DNA operations. One important operation is hybridization which is a main process in DNA computing to form all possibilities of solution strands in which the right answer lies. Hybridization is done by mixing strands in tubes with the help of some enzymes.

Apart form hybridization, the basic DNA operations available on DNA are mainly the following.

(i) Merge. $m(N_1, N_2) \triangleq N_1 \cup N_2 = N$.

(ii) Amplify. *Duplicate* $(N_1) = N$.

(iii) *Detect* (N).

(iv) Separate or extract. $N \leftarrow +(N, w)$, $N \leftarrow -(N, w)$. Given a word w consisting of strings from $\Sigma = \{A, G, C, T\}$ and a tube N, generate two tubes $+(N, w)$ and $-(N, w)$ which contain and does not contains the string w.

(v) Length separate. $N \leftarrow (N, \leq n)$. Given a tube N and an integer n, generate a tube containing stands with length less or equal to n.

(vi) Position separate. $N \leftarrow B(N_1, w)$, $N \leftarrow E(N_1, w)$. Given a tube and word generate a tube with stands beginning (ending) with the word.

3. Grid-Based Clustering

The grid-based clustering uses a multiresolution grid structure, called cells, which contains the data objects and acts as operands of clustering performance. Traditional approaches include STRING WaveCluster, and CLIQUE [8]. The most common grids are regular hypercubic grid. This requires that the grid construction covers all the data space with the same precision. The second method uses flexible grids, that is, multiresolution grids with hypercubic or hyperrectangular cells having randomly oriented borders [14].

3.1. A Flexible Grid Definition

Suppose that the data set is $\Omega = \{x_1, \ldots, x_N\} \subset R^n$. It is bounded by a rectangle D_0 in R^n. A grid is a undirected graph $\mathcal{G} = (V, E)$ where each node of V is called a cell and is represented by a quad $v = (D, c, p, \sigma)$, where D is a polyhedra, c is a center point of D, $p = |\omega \cap D|$ is the number of points of Ω covered by the cell, and σ is the diameter of D. We will always assume that a cell is nontrivial; that is, D has interior points in R^n. For a cell $v = (D, c, p, \sigma)$, its boundary is denoted by ∂D which is the set of hyperplane pieces bounding the polyhedra. If $S \in \partial D$ and S is part of a hyperplane H, then H is called a *tangent plane* of the cell. Two nodes $v_i = (D_i, c_i, p_i, \sigma_i)$, $i = 1, 2$, are called *adjacent* if the two cells share a common tangent plane and $D_1 \cap D_2 \neq \emptyset$. For two adjacent cells, define an edge between them. Hence, $E = \{uv : u \text{ and } v \text{ are adjacent}\}$. Figure 3 presents an illustration of tangent plane and adjacent cells.

To construct the graph $\mathcal{G}$, we need two parameters p_0 and σ_0 indicating the minimum number of points to be considered, and the minimum diameter. Then the graph is constructed iteratively. We start with the first node $v_1 = (D_0, c_1, N, \sigma_1)$, where D_0 is the original rectangle, c_0 is the center of D_0. Then at each step, the cell containing dense points (controlled by a threshold value p_0), or with larger diameter (controlled by threshold value σ_0), is split into two subcells by a hyperplane. A cell is sparse if it contains less points than p_0. It is called a small cell if its diameter is less than σ_0. If we reach a sparse or small cell, then add this cell to the node set of the graph. This step continues until no more cell left to be split. The resulting graph is called a flexible grid. Algorithm 1 gives the algorithm for the graph construction process.

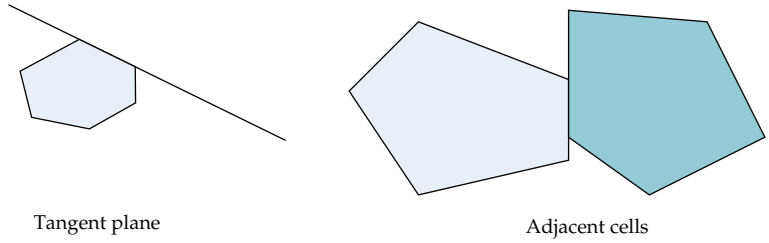


Figure 3: Illustration of tangent plane and adjacent cells.

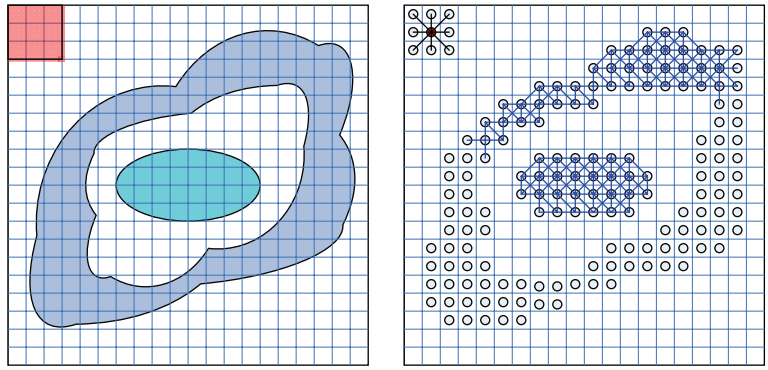


Figure 4: An example of flexible grid with induced graph.

We present an example to show the data set and the flexible grid generated by the above algorithm (Figure 4).

Next we define the weights on edges. A weight on an edge is the dissimilarity of the adjacent nodes. Suppose that the Euclidean distance in R^n is denoted by $d(\cdot,\cdot)$. Here and after, we will always assume that a data point $x \in D$ means $x \in D \cap \Omega$. Then for two nodes $v_i = (D_i, c_i, p_i, \sigma_i)$, $i = 1, 2$, the weight is defined by

$$\omega(v_1, v_2) = \begin{cases} 0, & \text{if } \min\{p_1, p_2\} = 0 \\ \dfrac{1}{p_1 p_2} \min\limits_{x \in D_1, y \in D_2} d(x, y) & \text{if } \min\{p_1, p_2\} > 0. \end{cases} \tag{3.1}$$

3.2. *Clustering Problems*

When the graph is constructed, the clustering problem is converted into grouping nodes of the graph into clusters. Traditional techniques include the hierarchical clustering [8] For the purpose of this paper, we will give a different approach for this problem. First it should be noted that nodes corresponding to sparse areas are outliers. Therefore, in order to reduce computing complexity, we first remove all sparse graph nodes with corresponding edges. We still use $G = (V, E)$ to denote the resulting graph, where V is the set of vertices, and E the set of weighted edges. An example is shown in Figure 4 with part of its edges.

Inputs: $\Omega = \{x_1, x_2, \ldots, x_N\}$ dataset of N points in R^n, D: hyper-rectangle containing Ω, p_0: population threshold value, σ_0: cell diameter threshold value
Outputs: $V = \{v_1, v_2, \ldots\}$: set of vertices
Begin
$V(1) = \{v_1 = (D_0, c_1, N, \sigma_1)\}$. Let $t = 1$ and $D_1 = D_0$.
while $V(t) \neq \emptyset$ **do**
  for each $v = (D, c, p, \sigma) \in V(t)$ **do**
    Choose a cutting hyperplane L passing c. Cut the current cell v into two subcells v', v''. For each $v \in \{v', v''\}$ of the new cells, if $p_v < p_0$ or diam $(D_v) < \sigma_0$, add this new cell v to the node set V. Else add v to $V(t+1)$.
  endfor
  $t = t + 1$;
end
End

Algorithm 1: A flexible grid construction algorithm.

Now we consider the problem of weight computation. By the graph construction procedure, we know that any node will correspond to a cell with diameter no larger than σ_0. Therefore, the distance between cells can be approximated by $d(c_1, c_2)$, and (3.1) will be

$$\omega(v_1, v_2) = \frac{1}{p_1 p_2} d(c_1, c_2). \tag{3.2}$$

In this way we can significantly reduce the computing time without loss of much precision. Again we define a parameter $0 < \omega_0 \leq \infty$. We will eliminate those edges with weight $\omega > \omega_0$. If this parameter $\omega_0 = \infty$, this means that no edges are eliminated. Now we use $\mathcal{C} = \{V_q : q = 1, 2, \ldots, k\}$ to denote a clustering of the vertices set V of graph $\mathcal{G}$ for threshold values p_0 and σ_0. Next we will use $|V_q|$ to denote the number of its vertices. Define the energy of clustering as follows:

$$\begin{aligned} \min \mathcal{E}(\mathcal{C}) : \mathcal{E}(\mathcal{C}) &= \sum_{q=1}^{k} \sum_{\substack{v_i \neq v_j \\ v_i, v_j \in V_q}} \omega(v_i, v_j), \\ \min \mathcal{E}_{\text{int}}(\mathcal{C}) : \mathcal{E}_{\text{int}}(\mathcal{C}) &= \left(\min_{\substack{1 \leq i, j \leq k \\ i \neq j}} \min_{\substack{u \in V_i \\ v \in V_j}} \omega(u, v) \right)^{-1}. \end{aligned} \tag{3.3}$$

Then the clustering problem is a minimization of the energy functions. However, the optimization problem is hard to solve. We will present a variation in the following.

3.3. Path Clustering

Now we consider the graph $\mathcal{G} = (V, E)$ with weight matrix W. Assume that the number k of clusters is a positive integer. A Hamiltonian path $\mathcal{L}$ of $\mathcal{G}$ is a path that visited each vertex exactly once. Now we remove $k - 1$ nonadjacent edges from $\mathcal{L}$ and denote the result by $\mathcal{L}_k$.

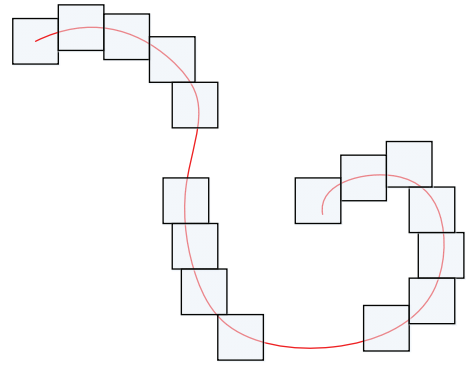


Figure 5: An example of path clustering with three clusters.

Define the energy $E(\mathcal{L}_k)$ of L_k as the sum of its edge weights. The path with least energy $E(\mathcal{L}_k)$ is called a path clustering

$$\min \begin{cases} E(\mathcal{L}_k): & \text{for any } \mathcal{L}. \\ E(\mathcal{L}_k): & \text{for any } \mathcal{L},\ 2 \le k \le N. \end{cases} \tag{3.4}$$

The first minimization of (3.4) is clustering for a fixed k, and the latter is clustering without fixing k. Path clustering is slightly different with distance-based clustering. The next example illustrates path clustering (Figure 5).

4. Clustering by DNA Computing

In this section we consider clustering of the graph $\mathcal{G} = (V, E)$. We still use N to denote the number of nodes in V, and this will not cause any confusion. Suppose that the number of clusters is k which is *a priori* determined, or defined in the process of clustering. The problem is to partition the vertex set V into k clusters. Suppose that the original data set Ω is bounded by a constant $M/2 > 0$, that is, $\|x\| \le M/2$ for $x \in \Omega$. Here we use the Euclidean distance for points in R^n and $\|x\| = \sqrt{a_1^2 + \cdots + a_n^2}$, where $x = [a_1, \ldots, a_n]$. Points in Ω are denoted by x_i and $\Omega = \{x_1, \ldots, x_N\}$. A point in the data set Ω will be denoted by the lower case letter x.

For each point $x \in \Omega$ and a cluster C, define the distance between them as $d(x, C) = \min_{z \in C} d(c, z)$ where $d(\cdot, \cdot)$ is the Euclidean distance. If C_1, C_2 are two clusters, then define $d(C_1, C_2) = \min_{x \in C_1\ y \in C_2} d(x, y)$. Clearly these distances are bounded by the constant M. For $u, v \in V$ define the *dissimilarity measure* as $\rho(u, v) = \omega(x, y)/M$. Clearly these dissimilarity measures are in the interval $[0, 1]$.

Now we convert the dissimilarity measures into integers. First we need to define an acceptable error rate $\varepsilon > 0$. This means that we do not distinguish those measures where their difference is less than ε. Now we divide the interval $[0, 1]$ into I subintervals with equal width $I^{-1} < \varepsilon$. For $z \in [0, 1]$ let its corresponding integer be $s(z) = [Iz]$ where operator $[\cdot]$ is the largest integer without exceeding it. Hence the dissimilarity measure lies in the set $\{1, \ldots, I\}$.

Now we define the weight matrix on the graph $\mathcal{G}$ by

$$W = [w_{ij}]_{N\times N}, \quad w_{ij} = s(\rho(x_i, x_j)),\ i, j = 1, \ldots, N. \tag{4.1}$$

A clustering of the graph $\mathcal{G}$, denoted by $\mathcal{C}$, is a partition $V = \cup_{i=1}^{k} C_i$. Thus any clustering can be taken as a rearrangement of the vertices $v_1, \ldots, v_N$. For example, the vertex set $\{\{v_3, v_2, v_1\}, \{v_5, v_4\}, \{v_6, v_7, v_8, v_9\}\}$ with three clusters can be written as

$$\mathcal{C} = v_3 v_2 v_1 \alpha v_5 v_4 \alpha v_6 v_7 v_8 v_9. \tag{4.2}$$

Here we use the greed letter α as a separator between clusters. Therefore, we have $k-1$ separators if we obtain k clusters. If we take dissimilarity measure into account, then a clustering will be as follows:

$$\mathcal{C} = v_3 w_{32} v_2 w_{21} v_1 \alpha v_5 w_{54} v_4 \alpha v_6 w_{67} v_7 w_{78} v_8 w_{89} v_9. \tag{4.3}$$

Now we have converted the clustering problem to a permutation problem. That is, any permutation of the set $\{1, 2, \ldots, N, \alpha, \ldots, \alpha\}$ (the number of α's is $k-1$) is a candidate solution. The string with minimum length is the optimal solution.

4.1. DNA Coding for Data

First we give the encoding of the dissimilarity measure, or the weights. In order to do this, we assume that 1 is coded by the string AG. And any integer $i \in \{1, \ldots, I\}$ is coded by seq(i):

$$\text{seq}(i) = \overbrace{AGAG\cdots\cdots AG}^{i \text{ number of } AGs}. \tag{4.4}$$

Next we present the encoding of a vertex $v \in V$. This is done by using a fixed mer sequence as the following example (20-mer):

$$\text{seq}(v) = 5'\text{-}TCTCT\ CTCTC\ TCTCT\ CTCTC\ TCTCT\text{-}3'. \tag{4.5}$$

The separator α is also coded with a single-strand seq(α) of the same length with that of points. This is done exactly as the data point coding except that we need to distinguish separators with data points.

4.2. Encoding Scheme

Now we need to put everything together for a candidate solution (4.3). First we design a code for an edge $uv \in E$ with weight w. This is done by linking the last half part of seq(u), seq(w), and the first half of seq(v) as shown in Figure 6(a). We need two special edges called the left half-edge and the right half-edge. The left half edge is a linking of seq(u), seq(w),

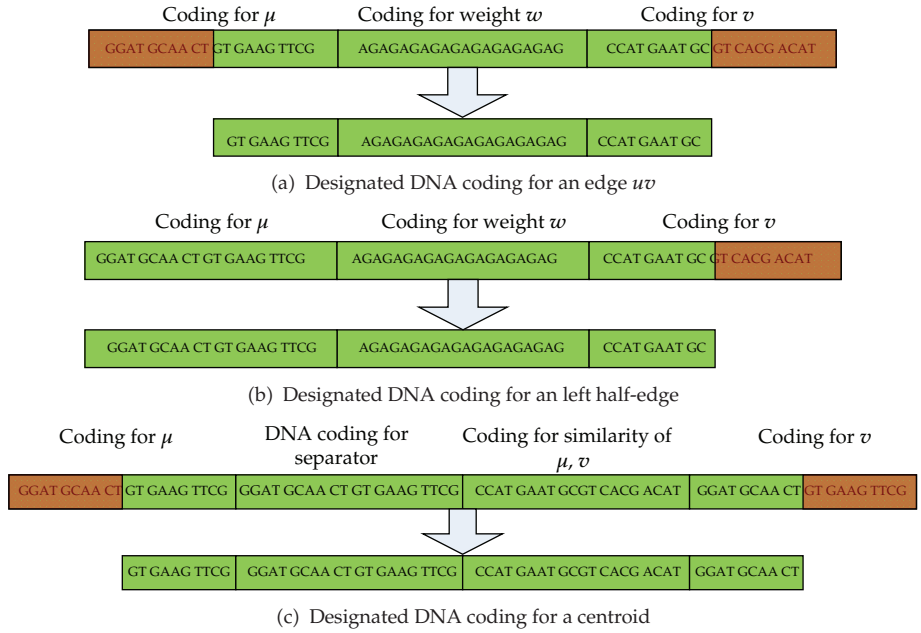


Figure 6: DNA-encoding architecture.

and the first half of seq(v). The right half edge is a linking of the first half of seq(u), seq(w), and seq(v).

Next we define coding for a centroid which is a complementary form of a separator α. First for two vertices $u, v \in V$, we define its similarity as $\hat{\rho}(u,v) = I - s(\rho(u,v))$. One should notice the difference with dissimilarity measure defined in the matrix W. Now we define the code of a centroid as a linking of the last half part of seq(u), seq(α), seq($\hat{\rho}(u,v)$), and the first half of seq(v) as shown in Figure 6(c). Here u, v are two vertices in V.

Finally, the code for a cluster C is a permutation of the following string without changing the position of the left half-edge and the right half-edge:

$$\text{seq}(C) = \underbrace{\overbrace{A\cdots C}^{\text{left half-edge}}\ \overbrace{A\cdots C}^{\text{edges}}\overbrace{G\cdots T}^{\text{centroid}}\cdots\cdots\overbrace{G\cdots T}^{\text{centroid}}\overbrace{A\cdots C}^{\text{edges}}\ \overbrace{T\cdots G}^{\text{right half-edge}}}_{N \text{ points and } k-1 \text{ separators altogether}}. \tag{4.6}$$

($N-k-1$ edges, $k-1$ centroids)

4.3. DNA Program

Now we describe the biological operations for the clustering. First we put single strands in a tube T_0 including complementary strands of all vertices, complementary strands of the separator α, and complementary strands of integers $1, 2, \ldots, I$. These strands serve as splints. We also pour strands into T_0 of all the left half-edges, right half-edges, strands of integers $1, 2, \ldots, I$, all edges, and all centroids. Then hybridization and ligation can be executed. As a result, all combinations representing clustering schemes are obtained in the tube T_0.

Step and Procedure
(1) **Input** (T_0).
All DNA sequences and complementary DNA sequences are placed in empty test tube T_0.
(2) **Amplify** (T_0).
Make all sequences in T_0 mixed together and execute ligation process. After hybridization process, all possible combinations of DNA sequences happen in T_0.
(3) $T_1 \leftarrow +(T_0, \text{seq}(\alpha))$.
Select only those DNA strands which include at least one separator α from T_0 and keep them into empty test tube T_1.
(4) **for** $i = 1$ **to** N **do** {**begin** $T_1 \leftarrow +(T_1, \text{seq}(v_i))$ **end**; }**endfor**; $T_2 \leftarrow T_1$.
Select all DNA strands that contain all the N vertices $v_1, \ldots, v_N$ in test tube T_1. Put them in empty test tube T_2.
(5) **Gel Electrophoresis**.
Find the shortest DNA sequence in test tube T_2. Put them in an empty tube T_3. This is the solution of clustering the problem.
(6) **Count the number of separators** α.
Amplify and count the number of clusters in tube T_3.
END

Algorithm 2: The DNA program.

In order to select acceptable solutions among these combinations, we need to eliminate those strands which do not contain a separator α and those which do not contain all the vertices $v_1, \ldots, v_N$. Finally, by counting the number of separators α as k of the strand with shortest length, we get the solution of the clustering problem. This final procedure can be implemented by direct observation to calculate the separator sequences by using special microscope such as atomic force microscope (AFM) to identify and calculate marking sequences [7].

The DNA program of biological operations is shown in Algorithm 2.

5. Examples and Discussions

In this section, we present some examples to illustrate the performance of our algorithm. Then we will show that our technique will give clusters more naturally.

5.1. Example One

First we present an example with 20 points to be clustered that is discussed in [7]. First we construct a grid with interval 1 as shown in Figure 7. Then we take $p_0 = 1$ as minimum points located in each grid. As a result, the induced graph is disconnected with 10 subgraphs. The final result shows four clusters with additional 6 outliers. This is different with result of [7] where they obtain four clusters with no outliers.

Now we change the grid into interval 2. Then we have only half the grids compared to grid with interval 1. We take $p_0 = 1$ but we use another parameter $\omega_0 = 1$. This time we surprisingly obtain three clusters (Figure 8) with two outliers. This fact shows that the clustering method proposed here is sensitive to the construction of grids and parameters. Considering various definitions and measurements of clustering, this is not too surprising.

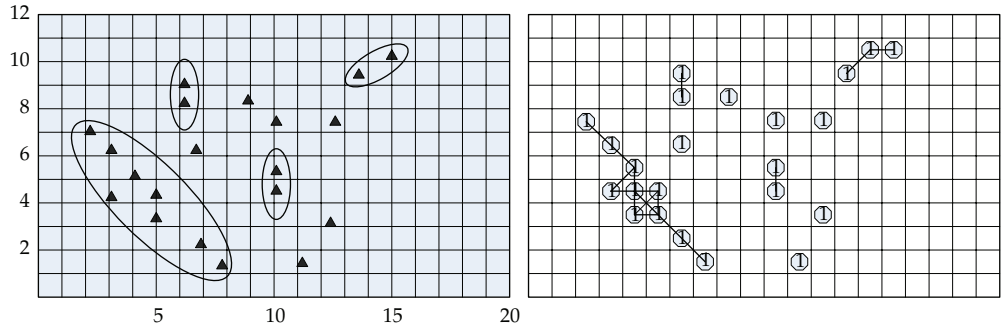


Figure 7: Data example one with graph generated with grid interval 1. Parameters $p_0 = 1$.

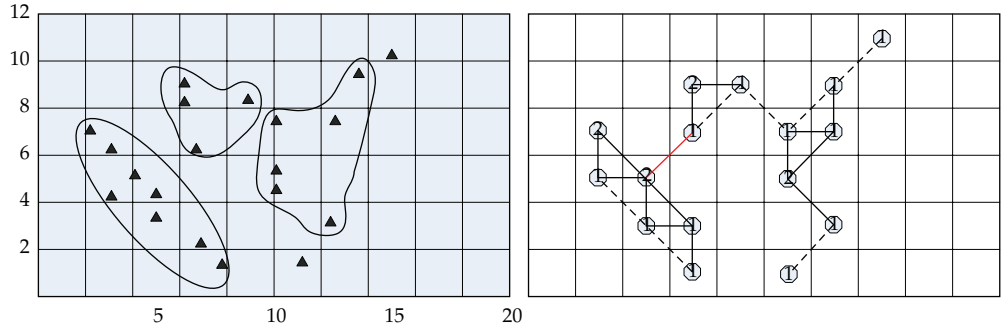


Figure 8: Data example one with graph generated with grid interval 2. Parameters $p_0 = 1$ and $\omega_0 = 1$.

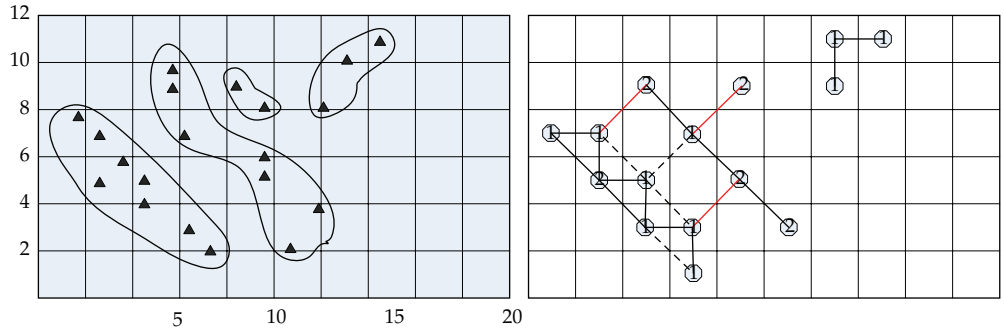


Figure 9: Data with different grid (interval 2). Parameters $p_0 = 1$ and $\omega_0 = 1$.

Now we construct a grid similar with Figure 8 but starting the first horizontal vertical lines not from coordinates $(0, 2)$ and $(2, 0)$. Identically, we can implement this case by moving the whole data set in the grid of Figure 8. With the same parameters as above, we obtain the third clustering result as shown in Figure 9. Now four clusters are generated without outliers. It is interesting to note that the three different grids induce one common cluster (left-bottom cluster). In fact, this common cluster is better organized than the other clusters. Hence we know that clustering is sensitive to the construction of grids especially for those *bad* clusters.

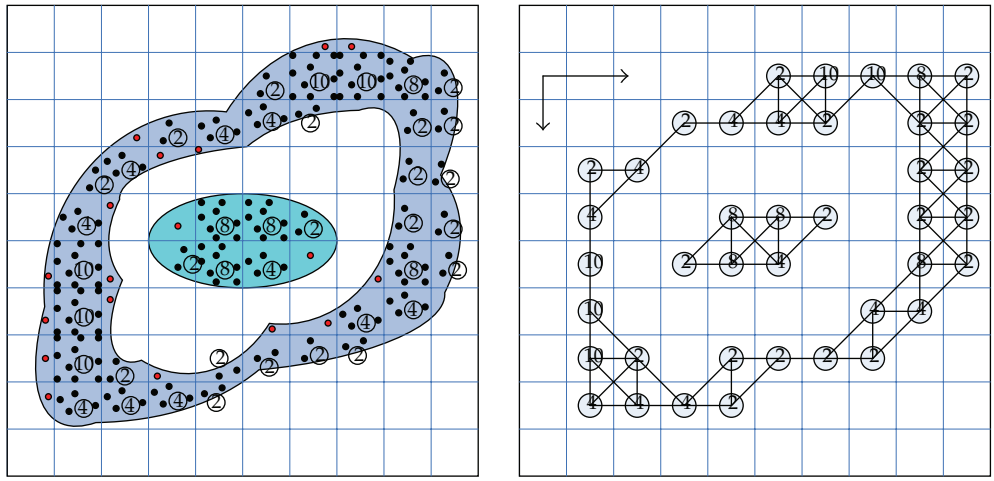


Figure 10: A data example with graph generated. The numbers in circles are the values of p in cells.

5.2. *Example Two*

Now we consider another example as shown in Figure 10 with the data to be clustered and the graph constructed. For this example, we take $p_0 = 2$. For adjacent cells, if they share a common edge, then we define their dissimilarity measure as 1. Otherwise if they share a common vertex, then define dissimilarity measure as 1.4. There are 40 nontrivial cells.

Since for any two cells $p_1 p_2 \leq 100$, we take $I = 100$ and by (4.1) the weight matrix is

$$W = \begin{bmatrix} W_1 & W_2 \\ W_3 & W_4 \end{bmatrix}. \tag{5.1}$$

Here W_1, W_2, W_3, and W_4 are 20×20 matrices, and W is symmetric. The matrix W_1, W_3, W_4 is shown in Table 1. The weighted graph is shown in Figure 11.

By the technique of this paper, the solution of clustering is a string. One of the clustering string as a clustering is as follows:

$$\begin{aligned} &v_{17}v_{18}v_{19}v_{25}v_{24}v_{23}av_6v_7v_8v_2v_1v_9v_3v_4v_5v_{11}v_{10}v_{14}v_{15}v_{21}v_{20}, \\ &v_{26}v_{27}v_{30}v_{29}v_{36}v_{35}v_{34}v_{33}v_{40}v_{39}v_{38}v_{37}v_{31}v_{32}v_{28}v_{22}v_{16}v_{13}v_{12}. \end{aligned} \tag{5.2}$$

6. Clustering of the Iris Data

In this section, we present another detailed examples to illustrate the encoding of the DNA-based clustering technique proposed in previous sections. The new example is the well-known Iris flower data set problem. The Iris flower data set is introduced by Sir Ronald Aylmer Fisher as an example of discriminant analysis [15]. The data set consists of 50 samples from each of three species of Iris flowers, that is, Iris setosa, Iris virginica, and Iris versicolor. Four features were measured from each sample, and they are the length and the width of sepal and petal [15, 16].

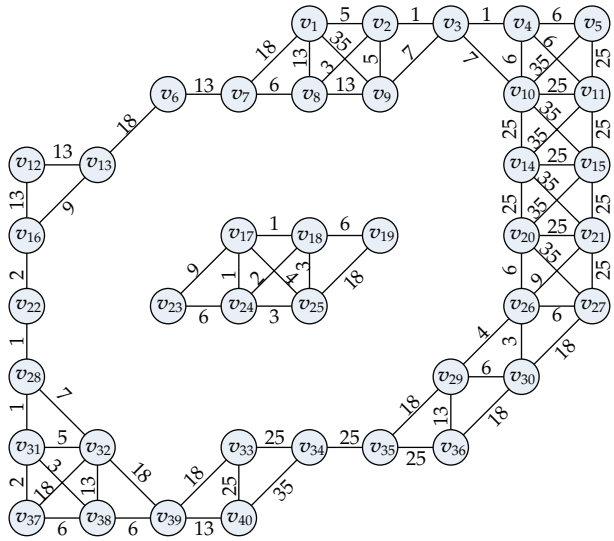


Figure 11: The constructed graph with weights on edges.

6.1. Grids and Graph of the Problem

Now we use a matrix $X|_{150\times 4}$ to denote the data set. Then X is located in a rectangle $[4.3, 7.7]\times[2.0, 4.4]\times[1.1, 6.9]\times[0.1, 2.5]$ which is in the four-dimensional space R^4. A grid cell (rectangle) D in R^4 has $2^4+4\times 2^3+4\times 2^2+4\times 2$ adjacent cells. If we choose $D_0 = [4.01, 8.01]\times[1.81, 5.01]\times[1.01, 7.01]\times[0.01, 3.01]$ for instance, then the grids are defined as follows:

$$\begin{aligned} g_1 &= [4.01, 4.21, 4, 41, 4, 61, 4, 81, 5, 01, \ldots, 7.81, 8.01], \\ g_2 &= [1.81, 2.01, 2.21, 2.41, 2.61, \ldots, 4.81, 5.01], \\ g_3 &= [1.01, 1.21, 1.41, 1.61, 1.81, 2.01, \ldots, 6.81, 7.01], \\ g_4 &= [0.01, 0.21, 0.41, 0.61, 0.81, \ldots, 2.61, 2.81, 3.01]. \end{aligned} \tag{6.1}$$

Then the cells can be denoted by $\mathfrak{D} = \{D_{pqrs}|_{20\times 16\times 30\times 15}\}$ with 144000 cells which is a huge number. Due to this reason, we choose x_2x_4 among the four dimensions as shown in the first image in Figure 12 as cluster feature variables. The second figure in the same image shows the other two dimensions x_1x_2 which is studied in Qu et al. [16].

Next we design a flexible grid structure as shown in Figure 13. Choose parameter $p_0 = 0$. Then the induced graph is shown in Figure 14. By (3.2) and direct computation, we obtain dissimilarities as matrices of the graph. Now we define the error rate $\varepsilon = 0.001$ and $I = 1000$. We cut the weight value by a maximum value 999. Then the weight matrices of $\mathcal{G}$ are shown as in Tables 2 and 3. Here we write the matrix as

$$W = \begin{bmatrix} W_{11} & W_{12} \\ W_{22} & W_{22} \end{bmatrix}, \quad W_{11}, W_{12}, W_{21}, W_{22} \text{ are } 13\times 13 \text{ sub-matrices.} \tag{6.2}$$

Table 1: Sample data weight matrix $[W_1, W_3, W_4]$.

0	5	0	0	0	0	18	13	35	0	0	0	0	0	0	0	0	0	0	0
	0	1	0	0	0	0	3	5	0	0	0	0	0	0	0	0	0	0	0
		0	1	0	0	0	0	7	7	0	0	0	0	0	0	0	0	0	0
			0	6	0	0	0	0	6	6	0	0	0	0	0	0	0	0	0
				0	0	0	0	0	35	25	0	0	0	0	0	0	0	0	0
					0	13	0	0	0	0	0	0	0	0	0	0	0	0	0
						0	6	0	0	0	0	0	0	0	0	0	0	0	0
							0	13	0	0	0	0	0	0	0	0	0	0	0
								0	0	0	0	0	0	0	0	0	0	0	0
									0	25	0	0	25	35	0	0	0	0	0
										0	0	0	35	25	0	0	0	0	0
											0	13	0	0	13	0	0	0	0
												0	0	0	9	0	0	0	0
													0	25	0	0	0	0	25
														0	0	0	0	0	35
															0	0	0	0	0
																0	1	0	0
																	0	6	0
																		0	0
																			0

0	0	0	0	0	0	0	0	0	0	0	0	0	35	25	0	0	0	0	25
	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
		0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0
			0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0
				0	0	0	0	0	0	0	0	0	0	0	0	4	3	18	0
					0	0	0	0	0	0	0	0	0	0	0	0	0	0	6
						0	0	0	0	0	0	0	0	0	0	0	0	0	35
							0	0	0	0	0	0	0	0	0	0	0	0	0
								0	0	0	0	0	0	0	0	0	0	0	0
									0	0	0	0	0	0	0	0	0	0	0
										0	0	0	0	0	0	0	0	0	0
											0	0	0	0	0	0	0	0	0
												0	0	0	0	0	0	0	0
													0	0	0	0	0	0	0
														0	0	0	0	0	0
															0	0	0	0	0
																0	0	0	0
																	0	0	0
																		0	0
																			0

0	0	0	0	0	9	25	0	0	0	0	0	0	0	0	0	0	0	0	0
	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
		0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
			0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
					0	6	0	4	3	0	0	0	0	0	0	0	0	0	0
						0	0	0	18	0	0	0	0	0	0	0	0	0	0
							0	0	0	1	7	0	0	0	0	0	0	0	0
								0	6	0	0	0	0	18	13	0	0	0	0
									0	0	0	0	0	0	18	0	0	0	0
										0	5	0	0	0	0	2	3	0	0
											0	0	0	0	0	18	13	18	0
												0	25	0	0	0	0	18	25
													0	25	0	0	0	0	35
														0	25	0	0	0	0
															0	0	0	0	0
																0	6	0	0
																	0	6	0
																		0	13
																			0

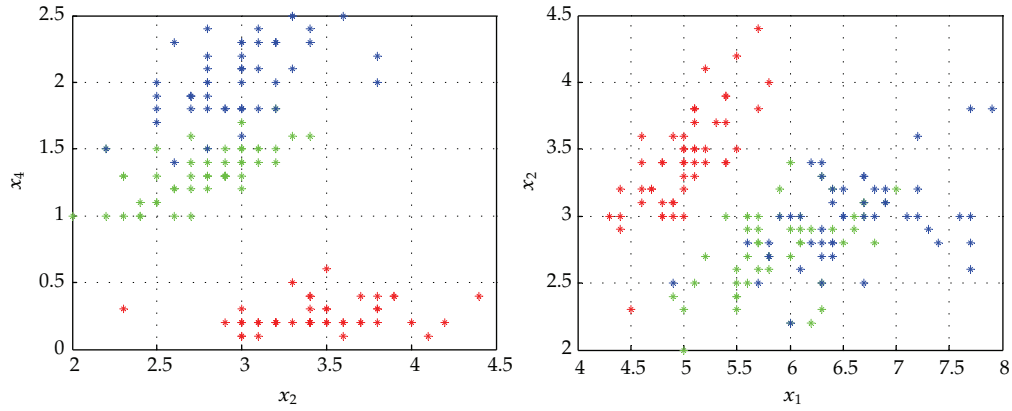


Figure 12: The Iris data figures for dimensions $x_2 - x_4$ and $x_1 - x_2$.

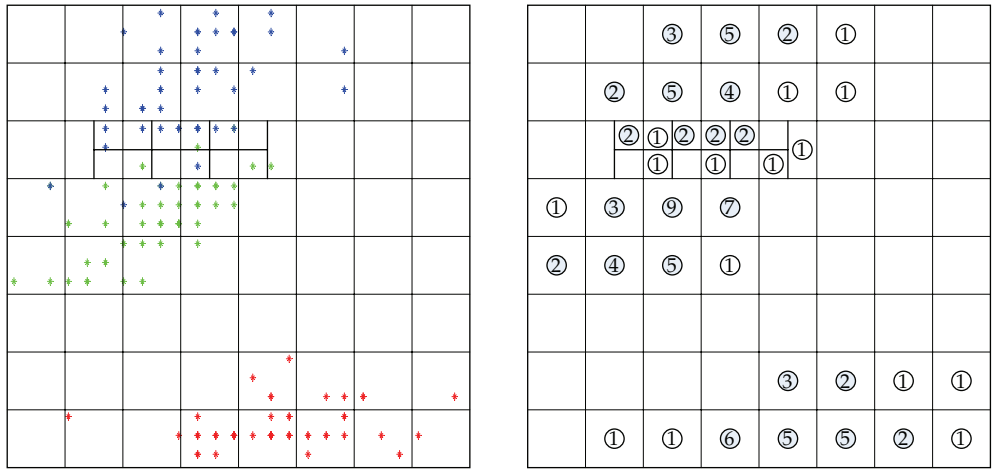


Figure 13: The Iris data figure for dimension $x_2 - x_4$ and with grids and candidate graph nodes.

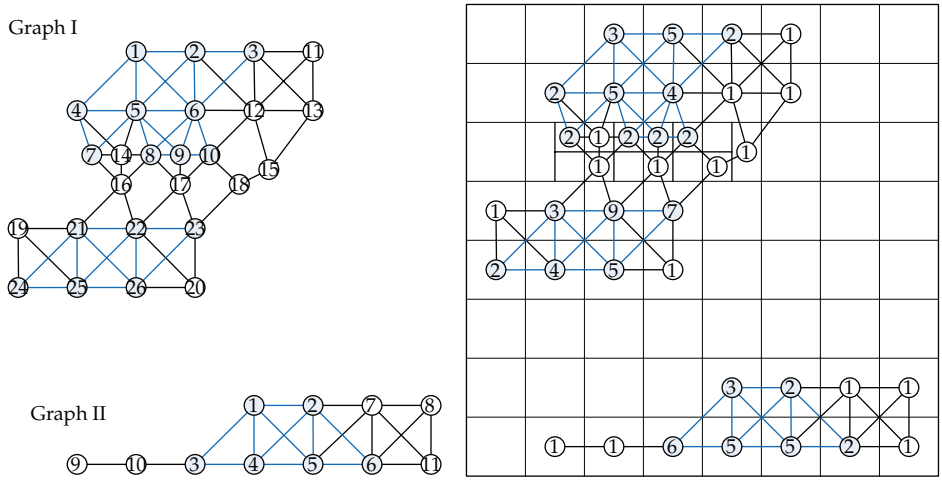
For the two subgraphs as in Figure 14, we can find Hamiltonian paths easily. For subgraph two, the path is

$$v_1v_2v_7v_8v_{11}v_6v_5v_4v_3v_{10}v_9. \tag{6.3}$$

There exists many paths for subgraph one. One shortest path with indicator α along the edge $v_{16}v_{22}$ as shown in Figure 15(a) is

$$v_{11}v_3v_2v_1v_4v_5v_6v_{12}v_{13}v_{15}v_{18}v_{10}v_9v_{17}v_8v_{14}v_7v_{16}v_{22}v_{23}v_{20}v_{26}v_{25}v_{21}v_{24}v_{19}. \tag{6.4}$$

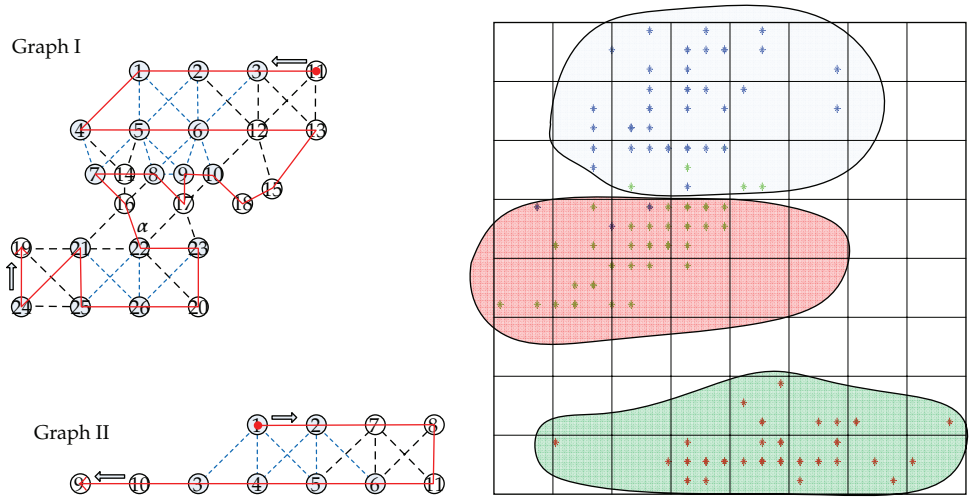
The detailed encoding scheme is shown in the Appendix. The final clustering result is shown in Figure 15(b). The number of points which is not correctly clustered is 7. Clearly this is much better than other methods such as CEPSO of [16] where the error number is more than 20.



(a) The number in node is its ID, and the number on edges is the weight value

(b) The number in the circled nodes is the population of each cell

Figure 14: The induced graph with weight.



(a) The shortest Hamiltonian path obtained

(b) The three clusters DNA method

Figure 15: A short Hamiltonian path for the induced graph.

6.2. Discussions

Now we present some discussions about the time and computational costs of the proposed technique in this section. According to Algorithms 1 and 2, the computational costs consist of two main procedures, that is, the grid construction and biological operations, and we will show that the complexity is roughly linear.

First we check Algorithm 1 for the construction of flexible grids. The time complexity is the total searching counts $\sum_{t=1}^{t=T} |V(t)|$ where $|V(t)|$ is the cardinality of $V(t)$ and T is the final t that $V(t)$ reaches null. Clearly $|V(t)| \leq 2^t$. Now we estimate the upper bound of T.

Table 2: Dissimilarity weight matrices W_{11}, W_{12}, W_{22} of subgraphs I.

0	67		236	67	118							
	0	100		56	50						283	
		0			177				500	500		707
			0	100		198						
				0	50	106	79	106				
					0		133	99	99		250	
						0						
							0	125				
								0	125			
									0		395	
										0	999	999
											0	999
												0
0												
	0											
		0										
530			0									
158				0								
					0							
250		354				0						
250		354	354				0					
			250					0				
			354	354					0			
										0		
	999										0	
	999											0
0	500											
	0			354								
		0					354	88				
			0					118	113			
				0					152			
					0		333			500	354	
						0		157	143			200
							0	37		236	83	94
								0	16		39	22
									0			40
										0	125	
											0	50
												0

In the worst case when $V(t)$ consists of 2^t cells, and each cell has a data population larger than p_0, we have

$$p_0 2^t \leq N. \tag{6.5}$$

Table 3: Dissimilarity weight matrix of subgraphs II.

0	167	79	67	94						
	0		141	100	354	500				
		0	33						167	
			0	40						
				0	100	183				
					0	500	707			500
						0	999			999
							0			999
								0	999	
									0	
										0

There we obtain the estimate $T \leq \log(N/p_0)$. And the total time upper bound is a linear time as follows:

$$\sum_{t=1}^{T} |V(t)| \leq \sum_{t=0}^{T} 2^T \leq 2^{T+1} \leq \frac{2N}{p_0}. \tag{6.6}$$

Next we analyze the complexity of DNA program as proposed in Algorithm 2. It is clear that the DNA program consists of three searching procedures. Step 3 selects those strands which contain at least one marker α which is a $O(1)$ operation. Step 4 checks if we get a sequence containing all the vertices with a complexity of $O(N_v)$, where N_v is the number of vertices and $N_v \leq N$. The final Step 6 counts the number of $\alpha's$ and splits the sequence into clusters. For the shortest sequence which contains all the vertices, the maximum number of markers α is N_v. Hence the total DNA complexity of the program is $O(N)$ which is linear.

Finally we make some comments about experiments. By Adleman [2] and Păun et al. [1], when we design a DNA program for solving the problem, a test tube (as taken in the laboratory) is considered a multiset of words (finite strings) over the alphabet $\{A, C, G, T\}$ with basic operations proposed as in [1, 2]. These basic operations are standard and biologically implementable.

However, when we want to simulate the algorithm with personal computers, there will appear some tricky complexity that lay behind the biological operations. Again we analyze the steps in Algorithm 2. First we consider Step 2, and we only consider generating sequences containing each vertex exactly once. The time complexity here will be $O(2^{N_v}) = O(2^N)$. By examining other steps, we find the total time is $O(2^N)$.

7. Conclusion

In this paper we presented a new DNA-based technique for spatial cluster analysis. Two examples are given to show the effect of our algorithm. We do not need the number of clusters in advance. By a flexible grid method we can reduce the size of searching space significantly. This is different with other DNA-based applications in that they enumerate all solutions which will produce a large search space. This is especially useful for large database even through DNA computing that has large parallel ability. Also by changing the grid and corresponding parameters, we can get various clusters.

Finally we will point out that nonconvex clusters can be easily obtained by the technique of this paper. Comparing to research in [7] where only convex clusters can be generated, this is useful for complex database to be clustered. Up to the authors knowledge, this is, the first research in cluster analysis by DNA computing for nonconvex clusters. It provides an alternative solution for this traditional knowledge-engineering problem, which is *not* a combinatorial in nature. Comparing the many applications of DNA computing mainly in combinatorial problems, this is still interesting.

Appendix

DNA Encoding of the Iris Data

In this appendix, we present a DNA-coding scheme for the Iris data problem. By Tables 2 and 3 the weight values range from 16 to 999. Therefore, we need a maximum length of 999 mer to code the weights.

First we present one coding scheme for vertices of Subgraph I.

VERTEX CODING:

1. GGCCCATT GTCGACGA 2. AAGCATCC GAACGTCT 3. ATTTAGTA ACTGTCAT 4. CCACTAGG CATTTACT 5. TAACTGAA TAGCCTAA 6. CCCATCCT GACTGCAT 7. GATGTGCT CGTAGCCT 8. AACCCTTA CGTGCATC 9. ATGCCCAA CATATAGG 10. TATTTAGT TGAAGCAT 11. TTCAGGAG GTGCACTA 12. CGTTTAGC CACCTTAG 13. TGTATACA CTTTATGT 14. CAACCATA GCCGCCGT 15. TCCCCGTC ATACCTTG 16. TAGGTATG ACTCGGCG 17. AGAAATCG GCCGCAAT 18. GAGCGACT TCCTGGGT 19. CAATCATT TGCGGAGT 20. GCCGTGAT ACCCTCAG 21. AATGCACA GAGTTTAA 22. TAGACTGT GTAAATCG 23. TCTACCGC CGTCCTTG 24. AATGAACA TTAGTGGC 25. TCTGCATA CGCCCCGT 26. AGCGTTGT GTCCTTCT

Since the edge coding of $v_j v_i$ is similar to those of $v_i v_j$, we next only present coding for one edge between each two vertices as follows.

EDGE CODING:

1-2: CAGCTCGT GGCCCAACGCCCATTTCGTACCACGAGAACCCAAATAACGGAGC-ATAGAAGGGCATCTTACTTGGAG TTGCTAGC 1-4: CAGCTCGT AGCTACACGAGC-TTCCGTATCGCTGTGTCGAATGGTGGGCCTTCTGTGGGAGTTAGGGGG CCGCTCAG-ACCCAGAATCGACCTGTTTATGCTGCCAGCTGTCAATGAATCTTAGAGTGTG AACG-ACATATCCTGTCGATTGTAG ATTGTTATCCTTGAAGAGATATACTTCGGCTTAGGC CTAGTTCGAAGGATCAAAACTACGCGTCAAAATCGGTCGCCGTTTATACCCCGTCC GGTGATCC 1-5: TTGCTAGC AACGCGCGGCCACCCTTAACTACCCAGTACCCACAT-CTCCTCTGGCATGTTGGG AAACTCGGGCTAT ATTGACTT 1-6: TTGCTAGT TACAAG-AAAGCATTAGACCACAAATATCACGCGATTAAATCAATGGCTTAA AATCGCTGAT-TCATCGGTTAACAGACAGCGCTAGGTTACCGTGATACCGTAGCACTCGATCTTAGTC TCCTAGGA

2-3: GTTGCAGA AAACTTGAAGAAGCGTCAACGAGTCGGACCTTGGCACTG-CTGGCGAGATCGCCGGACAAAATATGCATGTGCCCCCTACTTAAGGTAATCCGAT-TAGAGC TAAATCAT 2-5: GTTGCAGA CCACAGGAGATATGATATATCCTCGGCC-ACTGAGCCCTAGGCAACCCTGGTCTAAT ATTGACTT 2-6: GTTGCAGA GTAACCG-CGAGCCCTAACGCTTACTCTTTGACGGGAGTCACGAACTGACG TCCTAGGA 2-12: GTTGCAGA GGCACTTTGA GATGTCGGTG AAACTGTCCT CCGATCTCAA CACTAGT-GTG GAGTCTTCAC ATCACAATGG AACTCATACG GATAAGTCAG TCTGCCATGC CACAGGTAAA ATATGAGGCG AGGGCAG CTC TGGGCCTTTG TATCAGCCAG GTTC-TATTGT TTCAGGGCCC TGGTTAGGCT GCAATCAAAT ACCCATAGTA TTTCTGAGCA CAATTCCAAA TGACGCCCAA ACAGACGTGG ATAAATTGGT ATGAAGTCTA TGAC-CGTTAA ACGGAGTTAC TTC GCAAATCG

3-6: TGACAGTA GTTTGGACAA TGCGAACTGC GAGGTATTCA GTTAGCAGG-G TACCGACAGA ATATGTCCAG AAGCTT TGTT GGTCTAAAAA GTCACGGCCA A-TTTGCTAGC GCGGGCTGTT ATACGCTCAA GATGGGCACC AGATGATATC CTCA-TCATTC GGCCGCAAGT GACTCTTCGA TTATACT TCCTAGGA 3-11: TGACAGTA G-TCCAGGAAC CCCTTATTTT TTTGAAAGTT AACGACCGTT CTACCCGACG TTAGG-GCTGA CGCCTTCCGT ATACCAACAG CAAGATTACG TGATGACGGA CCAAATA-TA G CTCGTTGCCA CAAGGGTACA ACTAGGCTTC GACAATGTAG AGGAACGCA-A CGGGTCTGTG TCCTTCACAA ACCTACCTTT GGGAGGGTAG TGCTTGTTTT TAT-ATCTTTC TATGAGCCAG AGAGTCGATG GCCTGATAAG GCTGCCATCG GCTAAT-TGGG TACTTCGGCG CTCCCGAATA GCCCAATTGT GTCAGCGAGA TACGGCCCT-T GTGTTCAGCA TTGCCCTGTG ACAATTCATT GTACGACCGA CGCCCATCTA TGG-GTGCGGG GGTGGTTTAA AGAATTCTAG GTGCTACCTG CGACTCACCA CCGCTG-TTAT GACGGGGATA GTCGATACTA AAACTACCAT CATATTCATG CTCCGGAAG-A GCCGGCCAGT ATAGGTATTC AAGTCCTC 3-12: TGACAGTA CTCAACTACG TTT-AATTTAT GCGAAGCGAG TGATTAACCG AAGCGAAGGG TAGTACGGCT TCTACC-GCCA GAACACGTAG ACAGCGTGG G AAAGCGATAG TTGACAGCTA AGTCGGTT-GA GGCTGCACCC TGATGAACT C GTAATACATA GCTCAAGCTT CCATTGGTGG A-TTCTTTACC GTAGTACGAC TCACCCACAG GAGTCGACAC TGTTGGCTTC ACTTC-ATCTA TCCCAGGGCT TTCCCGTTAG CAAGGCATTA TTAGACAGGG TATTGCCGG-A CTAGCTAGCC TTAGCTATAA CAGGAAATAA TGCTGATTGG ACTGAACAGC G-ATGTGATTC CTCCAATAGC ATATATCCAT CGCCGAGTAT TCTTCGGTTG TTCGCG-CATA CTTCCTAGGA ATACCGCCGA TTATGAATTC GCCCCAGGGA GAGTCCGTT-C CGACCCATGA ATGATTTCAC CGGTCGCTGC GCTCGGTTCG TCATCTTGTG GCG-AAAGGTC GCAAATCG 3-13: TGACAGTA AAGAAGCTGG CCACATTCGT CACCTA-GCAT TGATTGGCGA TGTCGGTGAG GGAAATTGCC GCGGTACCAA GGCAGAACT-T GCGGAGTCCG GTGAAGTATG GAACGCGGAA CACGAGCCGT AGCTAGTTTG AT-GCTTTAAA AGCTTGAGAA ACAATACAAC CTGCCTGAAC CACGCTGCAG CAAGA-CGCGA GGCGCATTTA ATGGCGAGGT AACCAAGTAT GGTCCCCACC AGCTAACG-AG ATTAGCCGAC AGAGCATTTC TTTGATGCAA CGATTAACGC GCTGGTCGCA A-TGGTCCCAA GGGCGAGGGA AGCCCGGTTA TCAATGAAGG CCATTATGGG TAAT-CCCATA GACCAGGCTT GGTCAGAACC CTATCCTAGT AAGTCGGACG TTGGACGT-TG CAAGAGTGCG AAACATGTCC GCATAGCGTT TGTAAGAACT ATCGAGGAAC T-ACCTTTGTC GATTGTCTAG AACATGCCCA TGAAGAGAGC ACAGACATGC CAAC-CCCAAA TTATGTAGGA AGGGTACGGT TCTAAGGTAT AGTTTTGAGG TTGTTCTTT-T CGTCTACAGA AAAGATCCCC TCCGGGAGTA TAGTGCAAAA TCCATGGAAG A-GCCCACAAA AGTCAGAAAT AGACTAATAT TCCATGTTAT CAATCAAGTT AATG-CTTCAA CAAACCCTGA GCGTGCGCGA AGAAAAGTAG AGATTTA ACATATGT

4-5: GTAAATGA GAGAGGATTC CTGAGCTGTT CAGGCGGCGA GGCATCTAG-
G TGGTGCGGCA AAGAGATCTT CTTGTGTCCC ATCCCGCCCC TACCACTTAG ACC-
AAGACGA ATTGACTT 4-7: GTAAATGA TAGTGTGCTA GACATCTGGC CGCCGGCG-
CC AGCTCGTGGA TGCTCATAAG GCTTAACTTG ACGTCTTAGG AAGAAACTCA A-
GCCCAATCG CATTCTTCTT CACTGCAACA CGCGGTTGTT ACCGGCCTTT GAGTA-
TCTTT TACTTCGCTT TAGGCCCACC TGCAGTAACC ATCGCTGTCA GAAT TAGCT-
G AACTTTTG CTACACGA 4-14: GTAAATGA TGCGGGTGTC TAAGAAATTT GCATG-
AATAA GTGCTGACTA AGTTATACCG AAAAAGTCTT GCGGGACGCA GGTTGCTG-
TC TCGTATCTCT GAGAGCTCGT GTCCGTTCGG CCGGGACGAT AGGATGCCCC CG-
ACAATGAA CATGATCTTC GACCCACAAC GTACAAGACC CGAGCTAACA CTGCT-
CTAGT CATCCACGTA TTATTATTAC TACCACTAGC CAACGTGCAT CCCGCGTTG-
T AGTACGCAGG CTGTTTCACG ATGGCGATTT CCAACGGAAA GTTCTAACTT GA-
CAGCGTAC CACTAAAGGA CGGCCAGGCA TGGGCATCGC AGTTTTGAGT ATTCA-
CTCCG TGCACAACCG GACCTGACGT ACGTGAGGAC GAGGTCACCG GAACTAGA-
CT CTATCCTCCG CGGGCACGAA CTATTGACTT CAAACGTACG GACACCTATC TT-
AATAGAGG ATTTGACGCA TACTCGCTAG CTGCCGGTTG CCTCGGCGGC GTTGGT-
AT

5-6: CCGGGTAA CGCGAATCGC GGGTAGTTCG TATCGTTGGA TGACTGCAC-
T GCACATTTGC TCCTAGGA 5-7: CCGGG TAA ATGTCAATTC GGTAAGGACG TGG-
TGACATT GATGCATCTG CTCAGTGTGC CATATTCGTG CTCACTTCTT GCGCTATC-
TT TCGAGGGGTG TCACACACCT CTCAAG CTACACGA 5-8: CCGGGTAA GTCGCC-
CAGC TATCTGCCGC AGACAGGCAT ATAA CGGAAG GTATGGTGCC GTGCAGAG-
CT TTTGCGCAAT ACGCATGCA TTGGGAAT 5-9: CCGGGTAA GGCTCAGGCA CAA-
CTGAAGA TTGACACACG TATAGCCAGC CGACCAACTA ATCACCACCG CGTGGG-
CTGT CTCGATTTTG CCCACTATTT GCCGGGTAGA ACGCGT TACGGGTT 5-14: CCG-
GGTAA TTTCTAGCGG GCCGCCATCT TACTGAGTAG ACAAGGAGGG CATTCTGA-
AC TTTACTTCAC TATCGAAGCG AGCGCCGCGG GCTGACAGCG ACAGTACACA T-
AAACGTAGT ACGTATATTC CACCACAATG CCTTGCCACC GTCACCGCGA GTCTA-
GAC GTTGGTAT

6-8: GGGTAGGA TGTACCCTCG CGAGGGCGCC AATTGCTAAG TACAATAAC-
C CCACTGCTAG GCTATACACG ACGATCTAGC GTTCCAGTCG ACTCGCCCAG CT-
CACGATAA TGTGTACGCA ACAACGCCGC TGTCGAGCTC CAT TTGGGAAT 6-9: G-
GGTAGGA GCGCAAGACT TGATGAGTGA TCGTCCGTTC TGCCCGTGGA GATGC-
TGAAG CTCATACAGT ATGGCGCGCG ACAATCACTA TGCGGTGAAG TGTGGCCC-
C TACGGGTT 6-10: GGGTAGGA GTGGCCGGCT CCGCCAATCA GTCCACACGT TGA-
TGCCTCG GGACGACTCT CGCGTAGAAG AGTATGTACT GGGACCCAAA AAGCTT-
GAGA GGATTTCGA ATAAATCA 6-12: GGGTAGGA AAGGAGAGCT CGGGGGGGA-
T GTTTATGAAG AAATGCAGTC AATACACTCT AACATCCTAC CCGAACAATC AT-
GATTAAAC GTAGTAGTTT ATCCTATAAT TCGCTCCGCC CTTGCCCCAG AAGCGA-
TCAC CACCCACTAC AGTATACTGG GCTAACATAC GACGATTAAG TACCTTGTG-
C TAACCTCAAT TTCGCTACGC TCGTTGGGCT TATACCTACT AAAGCGAGGT CTA-
CCACCTA CCCTAAAAAA GCAAATCG

7-14: GCATCGGA AGTAAATCAC GCCTTCATCT GAAGGCGAGT CGACCTAC-
TT TCAGGTCGCT TTAGAATGCT ATATGAGATG ACGGAGGCAT TGGTTAAGTA C-
AACCTGACC AGCAACAACG AGTGGAACGG AGAGCGCGTA CAACTATATG TCA-
CCTCATC TAAAAGAGCT TACGAGTTAC TAATGTACGG TGGGGAAACG GCTGA-
GTCGC CCCTCCGGTT GCTCCCGGGT AGAAGCCGGA GACGAGCACC GTCCACA-
GGG GTTGGTAT 7-16: GCATCGGA TGAGCCAGGG ACTGAAACGG TACCACCCAG

TCGTGTGTTC TGGTATCTTG GGGCCGCCCT TATCGCAGCG ATGTCTCCAA GAAG-GTCGTC AAAAGCAGAT GGAAG TTGAT GCATTCTCTG GCCGTAATGT ATGTAGG-ATA ACCCCTTAGT TCCAAACTGC AATCACCCAT TGATAGTTCC ACATGTCCTG G-AATTAAAAA GGACCCTTAC ATCCTTAGCT TATGAGGTGC AGAATCCTTC TCTGG-CGGCT ATGTAGTAAG GTCACGAACG TAGGTAGAGA CAAATCCGAG TTGATTCG-CC ACACGTTGGC CGAGGCTCCG AGAAGGGGAC TTCAGACTGT TCTGGTTACC G-CTG ATCCATAC

8-9: GCACGTAG GAATGAGCTT AAACTAATCA GTAAGGACCA GTCGGGGA-AA CTCTAGCCCA TTGACCACCA GTTATTCTCG TCGGGTCGAG AGGCTCACAG A-TAATTTAGA TACCGAGAAG CGAGTCTTAG GGGAA TACGGGTT 8-14: GTATAT C-C CGGTACGATC AGAGACCCTC ACGCAGCAAC ATATAACAAT GCGGAAAATC T-CGTGTCTCA AATGCGTACT ATTCATATCT GTTGAACACT ACTAGGCCGA ACGC-AATGTT GTCAGGCCAA GCCACCGGCT ATAGGGATTT ATTTTACCCT CTTAGGC-AG G ATTAAATAGG GGCCAACCAG TTGCTGGGCC TGGGTATATG TAATGCCTA-A CCATAAACAG GAGGGAACCT GGGTTCAGCC ACACCATGCA GTCCACAGGG 8-16: GTATATCC GGAGAAGCGT GGCACCCTTG GGGGTAACTC TACATTCACC CAG-GAGG GCC TCTCCGCTTT CAACTGGGCA ATCTAACATG TGTCCACCGT GTACCG-GTAG CGCTACTGCC CGCTTCAAGA TGTAAGCGAG TACGCGTCAT CTGTTAGCG-A TGAGCGATTC TAGCGGGACG AGAACAATAG TAGAGTCAAA CGGCTTGGAG C-TAGAC AGCT TGTTTCTAAA CAACACTTAT CATTGCAACG GTGGGGGTAA GATA-TTCTTT AATGGACTCG CTAATATATG GGCCTGTTTA TGAGGACGCG GAACGTAA-AT CCACCAAGGT CCGCCGAGTC ACATTCTTGC CTATCGTAAG CACT ATCCATA-C 8-17: GTATATCC ACCTCGATGG ATTTCTGGTC TACCCAGGCA ATCGTTGATT CC-CCAATGGC AACTCCAGTA GGGTGTTACC AATTCGACAC CTCGCAGATC ACACT-GGCAC GGTGAGGCTC TCCGGCCGAT GATGGCAAAT CGGGTAATTC AGATGGGT-AC AATTTGTTGG AGAAAATCGT GGCGCTTTGC TTCGACACCT CGGGATCGGC A-AATCCAGTA GCGTGTATGC TTCGCATCCA GCGATGTAAC CATCCTTGAT TAGAC-GCAAA AGAAGATCAT GGACCGGTGC GGCGGGGATA CAATCGGTGT CTGGTGTC-GA CCGACTGGTC CACCATCCCC CGGTGAGGGT ACGCGGTTGA TGAA TCTTTAGC

9-10: GTATATCC TGGGAGCTGA AACGAAGTCG ACACACTCAG CTCACCGC-TA AGCTAGAGGG GGAAGTACCT TTGTATGATT CGGCTTGTCA GACTATCGAC C-AGGGCTAGG ATACTGACGG TGCAGATCAG GTAGC ATAAATCA 9-17: GTATATC-C GTACACAGCA GCGAGTCACA GACTCACCCC CACCCCAAAA GCATCGTGAT C-TGTTGCCGA CTTGCGTTTA GCGCGTAAAG TTTTTACTTA GTATCTTACT CTCATG-TAGC GTTATAGATA GACAATTCAT AGATCAGTAC TACAACGGCC CAGTTCT TG-C AGCGGATTGC CTATTAAATT CGGACTTGTG AGATTTGATG ACCAAGTTAT AA-AGGGTTCG TATTTGCAAT TCGCTGGTCT ACACCAAGCG TCTTTAGC

10-12: TCCTAGGA AATGTCCGTT CGGCAGGTTC TACGTTTAAT AGGTACGT-CG GGTGATTTCA CTATCCGCGC TCACCCTAGC CATATCGATC TCACATCGAT C-CGGTTAACT CGTTGCCCGT GCGGGAGGCT GCCGTTTCGG TAGGGTAGCA CTTT-G AGGAA GAAGCAGACC GAACACTGAG TGTCGAGACC CATAGCTGAA TTAAA-GCGAG CTTAGGGTAG GTGACAGCTG CGG GCCAATT TGGCAGCGTC GGACTGA-ATG ACATGGAACC GGCCTGAATC TGCGTGATTA TGAAGCTATC GCTTCTGGTTT-CTCAAAACA AACTCTCAGA TGTGTTGCAC CCACAGGTCG TCCTTGGTCC CGAAT-CCAGC CTCATTCTTG GGATCGACTT AGAGGTCCAA AGCTT GCAAATCG 10-17: T-CCTAGGA CCCAACTTAC ATAGGGATCA GAGTAACTTC ACCTGCTACT CTAGAG-CTGT CAGGTACGCC CACTCACGTG AAGCACACCA GTTTACTCGT CTGAACGTTC

GACGAGATAT TCGCCGGTAT AGATCGCGCC CTTTGATTTC TGTGCTCCCA AAAA-
GGATTT AGGTGTCAGA ACTGGTACTC CCGTAACGTT GGCTTTTAAG AGAGGTG-
CGG CTGTTCGGGA CCGTTCGTCG TGTCGCTCCA GGGTTCCTGG GTCGACATTC A-
GGGAGAAGC AAACAAAA CG TGGAAAAATG AAATCGCATG ACTTGCATGT TAC-
TTATTTG CGGGACGAGA TTTTAAGGAA ATTGGTACCT CTAG TCTTTAGC 10-18: T-
CCTAGGA GATTACACCA CACGTACACA TAGCTTCCCA GATCCCTCAG GTCAGC-
TAAA TGACGCCCCC ACAAGACGGC TACGCTTACC ACCAATCGTA TCCGCGTGC-
A GTCCAGATGC GGCCCACACA GGCATCCAGA AACTAATTTG ACGGTTCTAC C-
ACGACTGTC GAAAATTGCG ACGCCCAATT AGAACAATAC CGTAGACCGC GCGT-
TCTTGT CTAATTCTGT TTCCTCCGGA AATTCCATAC CGTTGGATAC TCCGCCGTT-
A AAGGGGTATG CTTCCGAACC AACAAAGGTA GATAAACGCG ACACCACGGT C-
TATTATACA TCCCCTGGCA ACCCCGGGCA CATCGCTCGT TTGA CTCGCTGA

11-12: CACGTGAT TAATATACAA AGACAACACT GGCATTCCAA GTTCAGT-
TCG GTCAACAATC CTAGATGGGG CGAG TTCATG ACGTGGAAGC CCATCAACA-
G CTGCACTTCG GGCAAATATG GTGCCCAAGG CTAGTCGCAC ATTACGACGA G-
AG AGGCACT GCCCTAGACC CAGGCACAGG CGAAGGAAAG CGCTCTGCCG GC-
GACCATAT ATAAATGACG GCTTAAGGTG GAATGACATA AAGCCGTCCC CCCA-
ATCGGC TTATATGCAA GAGTACTGGC ATCAATCCTT TAGAGGCGTG TGGGACT-
GGC CGGTAAAATG GCATTTAGCC GAACTGACTA CCGCACCAGA AATGACTAG-
T CTTCAGTAAT CGTTTTCTTT ATCACAGGAC GTTCCTCTGG GCAGATTTGT CAC-
GGTCCGC GACGCGCACT TCTGGTATAA TACTATGATA TTGGAAACAA CATGCC-
AGCC TCTACGCGCA CTTGGGCAAA CAAGGCTTAG GTCCAGATGA TTTCTCTCC-
A CGAGCACACC TGCCGTAAAT GAGAGATGCG TTTAGGAGTC GCACCTATAG G-
TCCTCTGCC GCACGAGAGT GTTTATTCCT CGCTCTGATT TCGAAATATT TCACA-
AATGT TCTAAGCTGC TTATGCTTCG TGATTTGACC CCCGTTGGTT AGCAGAATC-
T GCAGTCAATG AAGCTATTCC TCCATTCACC TGCAAAGTAA ACAGCGGGGT GA-
TTCAGGGA TGCAAGTCGA TGGCCTAGTA ATGTGAGGTT TGATAAGTCA ATACTT-
AT CG GAGTATCATT ATTGCTTTTT GACCCCTTGG GCGGACAAGA ATCTACAAC-
G ACGAACCGCA AGATAACGTT TAACTTACAT TGTTCACGTG CGCGGCCGGC AA-
AATATACG CGAGAAAGTC AGCTGTGTTG GGCAACCGGC CAAGGACTTG GACG-
CACCTC ATCGCAGCTT CGCACGTAAT TGGAGCGACT GTCAACTCAA TAGGTGC-
CCG TAACTCTGC GCAAATCG 11-13: CACGTGAT TGTATCTCGC ACACCGTTTA A-
CGTCTACCT TAGAACCCCC TGCTTTGCAT CATTTGTCTG AATGGCGGGC GCGAT-
TGGGA GTTCGTGTTA TATAATTGCA GTCTGGCAAT AGAGATTTCG CGCAAGAA-
GG TACAGGCGCC CGACGCCCGC ACGCCCTCAC ATACCTTCTC TGTAATAGCA A-
CTGTCGCTC CGGAGCTCGG GATTGTACCC ACATGGTTGT GGTCTCTATG GCGGG-
GAAGA GAACATGACC TTTGACCTGT GTCCCGTAGC ATCTTGGCGT TCCTACTTG-
A GTGGATATTG ACCGAATTAA GACATACAGG TAATCTCGGC CGTTTGGAGC GC-
AATCCGCC GCTTACATTA TCAAAAATGA ATGCCCGGTA CCACATATTC GTCCC-
AGGGT CTTCTAGACC CCGTCCTGTG TATAACCGAA CCTCAGAACC AAGACCGC-
CT ACTACTGACA ATCCTGCGCC CAGAGCATCC CTAAAAGTGG TATTCTAAGG A-
CGCCGCGCT TTACGATTAG CGCTCATCGT TGTATTTAGT TTAAAATACT CTTAA-
GCGGT TGATGCGTAG GCCGCAATGG TTTCGCAAAG GCGTGGCACT GAGCTGC-
TGA ATAGTTGGGA GAGGCAAA GT GGAATTTCTG TTCCAAGCGC CAGGAGACC-
G CCAATGGAGC TTTCATTCCC AATAGGGACT TGATAATAGT CGGCGGCATA G-
AACGCTGGA TACAGCCATA TCGCCTGGCC TCCAGCCAGA AATCGTGCGC CAGT-
AGTTAG GCAACTCACG TTCGAAGAAT TGGACCTCTA GTGTGGCTGA AAGCTCG-
GCG CCACCAACAT GCAATTACTC TGCCCATATG CAGTCCGCCA TTGGCCCTCA

ATATACCCAA GACAAGGGGA CGGAGATGAA CTCCACTGGT CGGCCACGTT CGAGGGGGGG CATTGCCGTG TGGCATCCGA TGGGTTCGCT TCTACCCTCG AGTGTTTACC CAACGCTGTA CTGGGGTTC ACATATGT

12-13: GTGGAATC AGGACCGCAC GGTCATTTGT TATTGTAACA CCTTGACAGG CGGCAACGGC TCGCCGGCAA GATACGCGAA GAGGAAATGG CGATTGAGGA TCTCAATTCA CTGGCCCCGA CTCCAGTTAC TGCCTCGATT TAGCTATGTT GCGAACTACA CGCGCTAGAG CAGCGTAGAT ACAGCTGACT CCCCTAAGCT GTTCCCGCGA AGCGTTATAG CGAATTTATA GC TCGGGCAT GGTGGATGGA CACCGCCCGG CTGACGCGTG CCAGGCCATG CAAGTCAGGC TTCTTGTTTG AGAACTAAAT AGCATCACAC CAAAGCTAAA CGGTCGGTGG GGTGGTCGCA TGTGCCTAGT CCTTCATGAA TGGATTCAGG CTATTTCAAG AGTTCCCGCG CACGAGGTCG CGATGTATAG GGGTTAGCAC CCATCACACG GAATCGGTGT TCTGACTACT GGAACGGTCG CCAGATATTC GTTGTACCGT TGATAACGCT ACCGTAATCA CCATTACCCG CACCACTACG ACAGGGGTTG GTTTTGCTCC CAGGTTTGTC CGGGGCGTCT GCTAATAGCG GCCTGGCAGT TGTCTAGTTA CTAGTAGCAT GGATACGTTT GGAGTTACGC GGCGTTAAGC TTTATTGGTC GTGGGCTCAA CATCGGTACC ACTGCGGCCC CACCAGGCGC CGTATAGCCG TGGGGGGATG AGGATTCTGC ACTACTGTAG TCCGACAGGC AGTGCGGAGG AATAGGATGA AGGGCGACCC GAGTTCGTCA AAATCCGCAC ACTATCAACT GTCCCCCGTC CCTTGCTACG GTGGAGGGGG TAATTCATCC CTGAGAGCAT AAGCAGTCAG TCAGGC TCGG GCCGGATATC GCATCGATGT ATTCCGCATT CTTGCTTCGC GGGGTGTCTG AAACATCTTG CGCCCCCAGC GACAGAACAT TATTCAAGTG GAAGCGGGCT CCAACCAGAA AGCAAACGGA ACGAAGGGCC AGCTATAGG ACATATGT 12-15: GTGGAATC ATACTAAGCA CCCTAGTTTA AAGAGTACCG CCGAAAACAT TGTTGAGGAT ACACTGCGAA TGCTGATTGA GACGGGAACC TGCGACATAC GGAACCAAGG GATCTCTATT AAAGCCGCTC GCTACTGACT AGATCCCGTA GATGTTACGC GACCTTAACT CGCTGATAGG GGATTCGCCG TGGGCGTTGT ACCACTGCGC CGACTTCTCT GCCGGCGCCG CCTCGGGTAA GTAACGGTTA GTAAGTGCAG TTGGTTTGGG CCGCATTGAG TGAGGTGCCT GCATGGTTTG ACTCTCATAT GCCTTGGGAG GACAAATTGA TCCCAGCAGA ACCAGATTTG TAGGATGATA GTTTGATAAA CACGTGAACA CTCCTCTATA AGTGCGCTGA GGGTGTCAAC AGACTTGTAT TAGGACCGGG GGCACACATC CGTTCATATG GCGTGGACCT AGCCCGAGGT TTTAGGTTAG TTACCCAACT AAACGCCTCA CATCTGATGA TACTTACGCA TTGCCTGACG AGTTGCGAGT TCTAGGCTAA AATAAAGATG TCGACAGTCG GTGGGATAAC ACTTTGGTGT GAGCGGATAT ATCAGAATGG CGGGACCATC TGGGATAAGC CCTCATGTTG GGACCTGGGC TGTCGAGGCC ACCTGCATGA ACTGCAAGTT TGACTACGTA GGCATTTGCC GCCCGTTTGA ACCAAACCGG CACTTACTAC TTGCGAAAAA AAACGAGTCC GAACCCAGCA TCGATCCGTT GCTACGGTCG AGTACTCAAT AATGGCGCTA AAATAGGTAC CGGCATCGTA GCCCCCTCGG TTAGCAATTC TGCAGTAATT ATAATATGGC AATTGAGGTT GAACACTTGC TATGCGGACC TTTACGAAGT TATGGCAGCG TGCGGGTCAG CTATTTTGGT AATCGCCCGC TGGTGTCTGA CCGCTACACA AACCGAATAC CGCACAATAC ACTGCCACAG CACTACTATC AGACTAAGA AGGGGCAG

13-15: GAAATACA CCGCGTTCGC CTGTGCGTAA GTCTAACAAG GCCCCGCGAA CAAACTATAT CCAGAAGATA GGTTCCCAGC GTCTGCTAAC GAATGTGTTT TATTGACATA CCAGGCAAGA GCTACTCCCC CTCAGGCCTA TTGGGGTAAC GATGATTCGC CATTAGGCAC CCGATGACTA TCGTAGACGC ACACCGTCGT TCGTCTACTA GGACAGTTTT AAGATGCTCC TTGGTACCAA TTGTGCAATG GGCTGAATCT ACACTTCCTG ATCATGGACG CAAGTTATTC CAATTAGACG ATTGGTCGAA

ATCCTTCCAT TGACGACCTA AAGTGAATGC GGGTACCTGT ACGAACCTGT CCCCCAGATC AATAGGACGA ACTCCGCGAG ATACCTAAAC CAAGTTGTCC GCCGCGGCTC TTGGAACCGG GTTTTAGGTG CGCCAATACG TTCGCCGACA GCGAGTTCTC TTAGAGCAAA GACAACAATG CGTTGTGCAT ACCGAGCCAA GACTCCGAGG ACCACGCGTG CGTCAAAGGT CAAGATAGAT GCGACGTTTT TGACGTCTAC CAGAATCGTG GAAAGACACA TCCCGTGGCT GTTCGCCCTA GTTGATCGCC TCCTGCATCA TGGGATAATC TCTTTCAGCA CCACGCCGCC GCTACACTAA GCGCCTCACA GCCTGAATAC CCGTCTTTAA GCTTTATATG GTAAAATTAG TAGGCTTTAG ACTGCTTATT GCGCGCCGCG CCTCGCTGAA CCACCGACAA TTACTGCCGC TGAGATCATT TGTGTTACTT GAACCCAAAC ACAGAGAGGG ATGCCAATGT ACCTATAAGC AGTGATCATT ACGCATAGCA GGTAACGAGG ATACTGGACT TCCCAATTCA CACCCTTCAA GCGTTGGCGT GGGGGATGCG GCCTATGCAG GGCTGAAGTC TGGAACCCAA GAGAATTCCA AAGGGTATTG AATTGAGCGG TCGCGATCAA TAGTTTGTTA TTCAGGCGC AGGGGCAG

14-16: CGGCGGCA ACCTACGCAT CAATCCACCC AGTGCCTATT CGTACATGAC AGTTATCGTT TAAGATTCCG ATAAGTACCC ACATAGGGGG GGTTTGCCGA TACACGCCGG TTGCTATCGT CTAACATAAC TGTAATAATT GACCCCTCAG TGAGCCGTAT GCACGACTTC GAACATTTTT CGTGTTTTAG GTTTTGTCAC GACACGAAAA CCTGCAGAAC CACATGGTGG CAGAGCTTGC ATACACCCCT TGATGGGAAA GGACTCTAGC TCTTTATCTT GCTACGGCAC GATTCCCGTT TACCGTAGAT TTAGACCGCT TGACCTTGAG TTCCTTGATT TAGCAGGTGA ATCCATGCGA AACCCATGCA CGATTCCGTT CGTATCCCTA TATTTGTGTT ATGACACAAG TTACTCAGTT GTCGGGGATA CCGGATATCG AAGACACGAA AATCGTAGGC CTTCGTTTTC TGCTGACTTG TGAGCATGGC AGACCACAGT GAGGAGTGCC ATCCATAC

15-18: TATGGAAC TGACCTAGCA CTTCGTTGTC GTTAGCACGA GGGCTGGTCC CCTATTTTGA GCGACCGTGC GGCATGCGAA GAGACCTCAA GGGGTAGTTC GAAACGGCTT TAAGTTGAGT CTGGATTTGT TCCTCGGTAA TGTGACCGGG TTTATCATCG GTTTTACCGG ATTAGAGTTA ATGAAGAGCC AGTTCAAACC TGCTTTCACG AAAGTGTGGG AGGGCGCTAG AGAATAAAAG CCCTGAGTAT AGCCTTCGCG CGAAATTAGT TGCACCACTC GTCTACGCCA TTTCAACAGA TTAGGATCGT ATCCTTTAAT GGGGGATGGA GGTTTCATTC ACCGTTTTGC AAATGGCGGT CCGG CTCGCTGA

16-21 TGAGCCGC AACGACATAG CAGAAATTAA CCCCCTTAAA CGGCAAAACG AGAGAGCATT TTTTAAGTAC GAGCACGTAT TGTTATACTG TTAACGACTA AAGGCAGAGC ATCGTGCTCC ACTAGTCATA GGGTGCCAGT GTTCACACCA CTC GTGTGCA TTAAACGTCG CGAGATAATC CAGACTAGCA GTGTAAGCAG AGCCACGCTA GGGGCGGGTT CCGCGGTGAA GCGCTACCAG GTCGACCTGT CTACGAAAAT AAGTAGAATG GTGTGTCGTA TAAGACCATT TTGTAGAACG CCGGGAACGA AGGACAGCGA CAGAGGGGTA TGCTACGTTA ACTGCATTGG TATCGGAACC TGAG TTACGTGT 16-22: TGAGCCGC TAGTAGAACA TGCCCTAAGC TATGCATGCG CGCCAATGCG GCGACGGAAA CCACGTCGCC AGCTCAATAG AGAAAACCGT CCTCCGCC ATCTGACA

17-22: CGGCGTTA GAAGAATAGG GCTTATTCGC GGAGGGACGC TGGGATACCG TTGCGGGTAG CGGTTACGCC TACA ACAACA CATCTTGAAG TGGGATGGCT TGATGAGCGC TGGTGAAATT GTTTAGTA ATCTGACA 17-23: CGGCGTTA GGTGGAATGA GGTTTTTTGA GTAAGTCGTA CAGTGCCCTA GCGTTCGGCG TACGCCCGTT CAGCCACCAA CCAACTTTAC GGACCTCCAA ACTAGCAGCG TGGTCTTCAC GTT AGATGGCG

18-23: AGGACCCA GGTGGCGATG ATCCCCCTAT CCGCAGAACT CTCGCGCTTA AGACAGTCGA TTGGGCAGCA CAAA GTCAGG TCGACTAAAT CCGCGGCGGC ACCAACATAA GGAATTAAAA ATTTGCATGG TTCGGTATTA GGAATACCTA CATGATGAGT AA AGATGGCG

19-21: ACGCCTCA AAATCTAACG CCATTCGGGG TAATCGAAGC CGAAAGACAA TCAGCACCAA TCGGCAAAAA GTTG ATCCCT CAAACATACG AGCTGTGGAA ACGACTAAGG CGGTGCCCCG ATGGCATACT CCTCTTTAGA AGGTAAACGT TGAGCTAGCC TCGTTGGGAT TTGCCGTTTT TAAAAGGGGA GACTGTGTAC CAGTTTAACT CGTTGGTCGT AGTACTCCAT CCTCGGGGCA TCTTCCATGT GTGAGAATAT GGAGGAATGA GAGTACTAGG TCACTTTGGG AAGCAGCACC CTACAGAAGA GTCGATCGGC TCTGGACATA TTGTTGTGAA TAT TTACGTGT 19-24 ACGCCTCA GTCGACACTG CGTCTGAACG GGTTCTGGCC ACCACCGAAT CATTTTAATA AGCACACTCC ACCTGCGAAG TATCGATGCC CACCAGCTAG AACGACTCGC ATCAGTGAGT GTAGGGCCGC ACCGACCGAG TGGAAGTTCA GGCAGCTTTG CACCAAATCC CCTCCCCTGA CTGCGGCAGT CGAG CGCGTC ACCAGCTACC CATTTATATA AGCAGGGAGA CGATTATATG CGGATTCTCA TAATGCGACT TCCCCCGTAC ACCCTCGGAG ATAGGATCGG AGACTTGGGA AGCGTAGTCG TCTACAATAG ACGTTGTACA TGGTCGTCCG TTGAAGAGGA TA AACAATCC CTATACCTTA CTTGGCCAAA TGCGTTCATT GCGGGCCAAT TCGCGACCGA GCAAATAAGT AGTGGAATGA TCTCGTCCCG GTATTATCCC AGCCTAGCTT CCGTCTAGAA CGATTTGTTA GGTTCAACGT TAGTTCGCTA GTAGGTTATA TTACTTGT 19-25: ACGCCTCA TCGGCCCTTT GCGTACCGAA ACCTCCCGTT TTAATCTCGC AGTTCGGCCC GCGAAGGACA TCCTTCCCGG GGGTTCTATA GAACCTCATC AAGAACCGGC TCTGTGTAAG TCTCCTTGGT CTGGGCGACG AGTTACGGGT TGGCTTATGT CCGGTATACA AAAGTCTCCG ATGATGAGTC TTCCCTTGGT AGTAACTCCA TTCGGGGTCT ACCGTCGGTC ACAGCTATAT TGGCATTAGT TACGATCTCA CATGTCGCGT TCGTACGTTC AATATGGCGG ATCGAAGTAT TGCACCTTAC CGCAGACAGC GCAGGCAGAA GGGACATTGC CAATATACGC CACAATAGGC AATA AGACGTAT

20-22: TGGGAGTC ACAACGCCTC GAAAGTGGTA TTTCCAGTTG TTACGGAGCT TCGGTAGTAA AAGGGGTGGC CTGCTCAAGG TGACCCATGC GTTTATACGG AACAAGGACC AATGGTTAAA CAATGGGCCA GACGTGTATT TCGCGATTGT CCTAGAAGAG GGAGCCA ATCTGACA 20-23: TGGGAGTC CTTACACCCC CTCTACTACT CGGCTGAACA GCTATTCGGG AGGTGCATGA AGGAATCCAC TTTGGATAAG TCCGGACCCC CCGACAAGGC TGGTTCCACG CTACATGCGC TGACGTTCTT ATAGCATTTC GGCTACTGAA GGA AGATGGCG 20-26: TGGGAGTC AGGTGCGCGG ACAGATGGAG ATTTTGGCAC TGCCGTACCT ACTGCAGCCC CGTGTGCCAG AACTATTTTA TTGCGCAATC AGATATTACA ATTTAACGGG GCGAAGGAGG GTTCTTTCCC CCAAAAGTGG ACGAGATGAT TGAATTCTTA GGCTCCATCG GACGACACTC TTGACGCATA TGAACGCCTG TAGAAGAGAC TCGCAACA

21-22: CTCAAATT CCAACGACAT TAGGGTAATA TCCAATACTC TCATCGT ATCTGACA 21-24: CTCAAATT TTTGGTAA AG GCACCACCGG GACGTGAGAG TCCCCGAAAT AGAAGCTTGT TGTGGTGGGA TCCCTGCCCC GTGAGTATTG TGGCGAACTC GGCCTATGTG CTAGTACGCT TGTATCCCAG AGGGTTCCTT AACTGCCCAC TTGGAATGCC GAGCGAACCC CCTTATCTCC TGGATTGAGG AAACATCACA GGCATTGCGG GATAGGGTGA GATCAAGCGA TCCTTATGCG AGCCCA TTACTTG T 21-25: CTCAAATT AGGTACTCGG TTCTGACTTG GTAATAGCAT CGTACAATTT AGGTGGGAGA CAGTGGAGCT GTCTTTG CGC GAGAGGGTGT TGT AGACGTAT 21-26: CTCAAATT CAAGATCACG AAGTCCATGT TTAAATCCCA TTCCCTCTAG TTGC

GCACTA AGCAAAAACA GGCAAAGGCT CAGCAAGACG AGATTGTCGC TCTG TCGCAACA

22-23: CATTTAGC TGGAATAAAT ATGTAT AGATGGCG 22-25: CATTTAGC TGAGGATCAT AGCGGCACCC AAGAAAGAAT AAGGAATGA AGACGTAT 22-26: CATTTAGC TGGGCTGAAC TGTGCGTTCT CG TCGCAACA

23-26: GCAGGAAC GACGTGGATG GAGTGCGACA CTTCGTTGAT CAGTTATTCG TCGCAACA

24-25: AATCACCG CGCGGCTATG GATTGTGGGT AGAAATAAGA AGTTGCCACG GGCATCAACC AATACTCCTC AAGGACAATT TCGGGTCGTA GCTCTTGGTA TAGCTGACGA ACTAACCGTG TATCCCACGT AAAAG AGACGTAT

25-26: GCGGGGCA ATATAAGGAT GTGGGTAGCA CCAAAGACCG CAACTTGCAA CGCCTCCCTC TCGCAACA

Next we present coding for Subgraph II.

VERTEX CODING:

1. GTTTTACC TGGACAAT 2. CGCGTAAT CACACCCA 3. TAATGAGG ACCTGGCC 4. ATTACGGA ATAGCTAA 5. TCAAAACG CGTGCGTG 6. TGTTTATG TGTTTACT 7. TTTGACCT CGTAGCTG 8. TACCACGT GGATGAGG 9. GGTGTCGC CCAGCTTT 10. TAAACGGT GCACCTCC 11GGGAGCAT AGCCATTA

Finally the edge coding for Subgraph II.

EDGE CODING:

1-2: ACCTGTTA ACTGGAAACA TCATGGGTCC AGTCCCCACG GGACAGAACC GAGGGACGGT ATGAAGTTTC GCCAAGACGA GTCTTGCATC AGCTGATCTT GTAATGTTGA CCTATGTTAT GGGTCCATGG ATCACTACGA CCCCGAAGTG GA TTTGTTTT TGTGGCGTGC CGGTGTA GCGCATTA 1-3: ACCTGTTA TTGCGAACTT GGAATACGTC AATGTCTACG GGCATTGGTA ACTGTTAGCG CACCGTCCGC GACAGCAGCA TACGGGTGG ATTACTCC 1-4: ACCTGTTA GGGTTCGAAT ACCCCTATGT AGTCATGAAT CGTTTATCTA TTGTACCCTG AGTACGTATG GTAAAAC TAATGCCT 1-5: ACCTGTTA GGGTCGGTCA GAAGGTTTTT GTTTGCTGGT TCTGCCGCGT GCCCCCGTTG TTATACACAC TGGTGGACGC ATGTGCGCAT GAATGTTCAG CAGA AGTTTTGC

2-4: GCGCATTA TGGATAACGC GACTGTAGGA GCTGCAGGTT GACACGTTCT TACGGCTGCA CATATACTTA CCCTTTT CTC TAGAAGGCTA GAAATAGCTC CGTTAGCGCC GTCTCGTCAC GTAGTAACGA TGTCCGCATC TTAAACGCAT T TAATGCCT 2-5: GCGCATTA CATACCGATA CGGTCAAATC TGGCAGATGG CCGGCTCATA TCCTGAGGCC GCTCGAGCAT CCCACGCACA ATTGTGACCG AACGGCGTTC CCACGGCGAT AGTTTTGC 2-6: GCGCATTA GTGACACGCG AATAGGAAGA GGGCACCTTA CTGCGGCTTG GACAAGTCGT GACTCGTAAT GTTCTAATAA CCTAATTTTC CTCATGAGTG AGTTGCTGTT ATAAAACTTA CCGAATAGAA GCTATGTGCT GGGAACGGCG TGAGTATAGA GACCACTTTC CGGCGCATAC GTCCGCCGCG CTATTTATTC ACCGAAGACA CGGGGCATTT AGCCCGGAAT AACGCGATGA CAGGATAGTG TATGGGCTCT CACATTGCAT CGCAATGTTC ACATCGCGTG TCCCGTCAAG TAGGGTGCGA ACGCCATAAA CGGCTGACAC ATACCCGGTA CTAGATCACC GATTCATACT AGCT ACAAATAC 2-7: GCGCATTA ATCCGCAAGA ACGTAAGTCG AGATTGAGCG TAGATAACAC CGCAACGATT CGGCTGTTAC AACTTAGGAC AGTTTCTGGT TTCCAAGTAT TGTGCTCAGG TCATCGGATG GGACAGTCCT GGCGTCGAGG

CACCTGGTTT CCTGCTGATC GACATAACGT GACTTGCTGA TGGGCTAAAA TCAG-
TACCAA GTACAAATGA TGCCAAAAAC GATTCAGTCA CTATGCCTTG AAGCATT-
ACG CCCCCGAACG GGGTACAGAG ACCTCGGACA AGTGTTACAC GTCCAGTCC-
T GCGGGGACGT CAGTCTAGGG GCCCCTTCAG GCTTCGACCG TACTCAGTGA GA-
TGAACTCA ACTGAA TTTG TATTCCCCGC TAGTCGCTAT GGCGAGACTA GTAGGT-
TCCT CTGGCCATAC GTCGATACTA AGCATAGGAA TCAAACCCGC CGCCTACGC-
T CGGTATGCAA GAACCCGCAG CTCTATGAAC AAGCTCAAAG CCTGAGCGGC A-
AACTGGA

3-4: TGGACCGG GCAAATCTCA CCAACTTGAC TTACATTGCT GGG TAATG-
CCT 3-10: TGGACCGG GATTGAAACA TTTAGTGACT AACGGCGTTC GTCTTCATC-
T AAGACTCAGG TGTGTGTAGC AAGTTACTGC GTTTGAACGG CGGAAACCAA CA-
GCTGAACG TGTGTTTTGA ATGGTTCGCG ATATCACCCT TCCACAGTGA TCCCTTT-
TTG ACGAGTGGAC GGTACCC ATT TGCCA

4-5: TATCGATT GGAAGTCGTG GGCAGGTTCT CCATAGGATC CTTAATGAG-
G AGTTTTGC

5-6: GCACGCAC AGCCTTTAAC CATCAAGTAA AGAACAGTGG CGTCATGG-
CC GGCGGCTGGG TGTCCATGAG TTCGTACCGT GCTAGTAAAA AATCCTCGCG C-
CATGCACGT ACAAATAC 5-7: GCACGCAC TCTTATCAAT CAGAAGGGTT GGGCT-
GTGGC TCAATTAATC AATAACGTTG CTATCACCTG AGCCATTCTA AATGTGAAC-
C AGGTCGCTAG CTAGATCCTG CCTCATGTAG CATTTACACC CCTAACAGCA TA-
GCCCGCTG TCGGGTGACG ACGGCCGTAA ACGCGTGCCA AGAACGGTAG GCT A-
AACTGGA

6-7: ACAAATGA CCTGGGCGTC TTCGGCATAA CAGCGGGGAG CGCATACT-
AT TGAGGGTACA ATCAGGATCC TTTCTGGTTT TCTCCGAGTC CCCTGGTGCC G-
TGGTCCCGC ACGGGGGTAG TGCCGGAATG TCGCATAGGA ACGTCAGTAT CTG-
GG ACCGC CCCTAGGTCG GTGAGTCCAC CGTGTATCGA GTGACCAACC AGGCC-
CTTTT TACTAAACGG GTGACATTGT TGCCAGATAC CTTCATGTTG GGTTCAGCG-
C AAGCGGCGTA ATTGCAAATG TTGCCAGATC AATCTAAGAT CACGTAGTGA G-
TACG TCCAG CTCTAGAGCT ACCCTTCGGC TCTAGGAGCA CGTTGGACGC AGGC-
CGGAAT TACGCTATTA ACCTTGTCGT CCTCCAATTA CGAGCACCTC TCAAGGCT-
GA GTCGTCAGGA GGTGCGCTTT CCCTGGCTAC TGTGTCGGCT CGCTGAGCTT G-
TCTATTCGC CTGACTAAGC CCCCGTCTAA CTCAATATGG AAACTGGA 6-8: ACAA-
ATGA GGAGCCAACC CGTATCAGGT TGAGATGTGG TATACTTACG GCTGCACTC-
G TAGTTCCTAA GTATACTCGC TAACTTTGTC TCACGGAATC CACTTTGCCG AAG-
GAATATG CCTTGTAAGA CTCCCTTATA TTGAAGGGTA GAGAAGATTC TTCTCAG-
GAT AACCCGGAGG TACAACGCAT CGGTCGGCAA CCTAGGGGTC GACGACTTA-
C TACCGCTGGT ATCCTCTGCG CGTGGAATGG TAGCCCCTCG GCCGGCATAA GC-
AGACTACG GCAAACGGTA ACGTTCTACT TCGGGCGGAT GTCCATTGGA GCCAT-
TTAGG CTAGAAAGGG CCCAGCTTTA GATAGAACCC GTTGCATATG ACCTTCTC-
CT TCTAACGAAA TCTAAGGTTC ACGGGCCCCC CCTCAGCGAA CATGTCCCGC C-
ATTACTACA AGAGGCATGT TCGCAAGATC CAATTATTGG TGTTAACCTG GATT-
GGTGCC TAATGTATGT GGCCGATTTA CTTCGTTTCT TGCTTGCTGA GTGTGGTCC-
C CCCCGACTTC CGCGCGAAGT CAGATATCAA CATACGGCCC CCTGTGCCAC CA-
CTGGTGAC GTAATTAGAG GTCTAAGACT TTTGTGTTAC GCTCTCAGTT AGGGCC-
GACG CGGCATTTAA ACTTGGGAGG ATCGACGCAT CTATATCTGG CTCCTAATA-
C CATATTAGAA TACACAG ATGGTGCA 6-11: ACAAATGA TCACGCAAGG CAACC-
ACGGA CCCAAATTGC GAACCACCTC TGGCGAAGAC AAACATACAC AATAATT-
CCA TTCGCATGAA ACCCGAGCTT CGCGCCGAAT TAGCTGTAAG AGCAAAAATA

ACGCAGGCAG AGGGCGTGTA CCGGGGGCGT CCGAATTCTG GAGGCAGAAG TA-
GAGGTATG TCGAAAATCC ATTACCTCCG TATATTCACT TCCAAATAAA TAAGG-
AATCT AAAACTCGCA CCACGTGCTT TTTAGGTCTA CATATGTGGG CCGCCGAAC-
G ACCTGGTTCG TAGAATCGAA GTCGTCGCAG CAAAGACGCT CTGTT CGGGA A-
TGGTAGCAG GCCCTTTATA CGGTACTTTT ACTTAGGGGG ATATTGGCCG AGATG-
AGGTC CTGGCTTAGC ACCCCTAAAA GCAAACACGT GGCGGAAGAC AGCAAAC-
AGG GGGGTCCCAG TGAGATCCCG GGACTGCGTT AAGCGGGTCC CGGACTATC-
A ATCTAGTAAC CCCTCGTA

7-8: GCATCGAC GTTGTTTGCC AGCCGGAAAT CAAGGCAAAA AAGTTAGAG-
C CTGTATGTCA GTGTTATTCG TTATAT CTGC CTAAGCTTTT CTCCTTCGTA TGTC-
AAGATC CGAATAACCA AATGATTTAC TAAGTCTTCG CCGTTCTAAC ATGCTCCG-
CT TGACGTGAAC TTAGGCGTCG AACGAGTTGG CGACAGAGTG GATGGTTACT A-
TCAGTGTGT AGTCGTCGCC CCGTAGGACC CCATCATCAA TCCTCCCCTC GCGTA-
GCGAA CGCACCGTCG GGGAACGGGG ATTGCGGAAG CTTGCAGCCT AAATGCA-
TCT AGGCCATTCA CGAAAGATGG GGAGATGTAA ATGGCCTCAA CACAGTACC-
T GCATTGTGCT AAGGCAAATC GTCATTGGAA TACTCGTAAA GGCTAACGAC AG-
TGAGCAAC AAGGATTTTA TCGGACCTTT GTGCTGTGAC AATCTGAACG TTTCAA-
GCAA GAACGTAGGC GCGTCATGGA TTAGGTCCGA CTGTTCTATC GTACGCCGA-
T GTGAGTGGAA TTACGCCAGG ATGGCAGGCG CGAGCCGAAT TACTCGTTAC GC-
GATCCGTC CCAAATTGAT TGAATAACCT GCATGTAGAC CCACGTCCTC TCGGCA-
AGCC TGTTACGTGT TATATCTTTC TTTTCAGCAT CCTAGACAGA TCGTTAACCG T-
ATAGGGATA CTACAAACTC TGATTCATCA AGACCGATGA AGTTGCTATC CCAC-
GTTGCA CATATAAAGA GTTTCAAAGA GGCCCAACCT CTTCCTCCGT ATTCGCGC-
CA GTAACGGTCG TTTTACGCCG AATGTAATAT TGTCCGCGCT CCTACCACGG GT-
TTTACTCA AATCGAGCAC CGACTACGTC AACAAAGCTA ACTATGTGGA TAATC-
ATAGC GACGCCCAAA GATCATAGTA TTAACTCCTT AACTTTTTGC GGTGTCTGA-
A CACAATTGGG ATACGACTAT GGAGAGGCTC GGAGCGGAAA ACATAGCGG A-
TGGTGCA 7-11: GCATCGAC CAATGCATAT ACCTAACCTA AGGCCGATAT CCCGT-
CTGTT CCTCAGCCCT GGCTGACCTC CGCCCTGCTG GAGTTGCAAT TGGCACTAA-
T CCTTCATCGG AGAGAAGCGG CCCGGGTGTA GTATAGATGC GCTGCGAGTC AC-
AGGCTGCC CGTCGTAGAT GACGATCTTA TATATAGTCT TTCAGTGAAC GGTTCG-
CATG TGAGTTAGAC CCGTTTCAGC GCGCGGCACA TCAGTTTAGA ATGGCGCCT-
T TGGCTCGTAA CCCAGGTTGA GAGTATACTC AGGTTTTACA ATTCGACATC TTA-
ACTGATA CGTGATGGAT TGCCGCGCTG TTTTCGTTAA GCTCGATATT TCACGAC-
TCC TATACTAGTT CGAAATTCAA TCACTGGGAA GGGTACTGGG CATTTCCTAT T-
ATACCTCTA AGAAGTACGC TAACAGGCGC AAGTATTGGC CTACAGACTT TAGG-
CGCCTG ATGACAAGCC GACTCCCCGT TTATTTAGGA CGCAGAAGAG TTAAGTC-
ACT TCCCCCTCAT CTTAATAGTG TATGATTGAC ACTGAGCACT TTACAGCGGT T-
ACCGAGTTA GTGAGATACG GGAATACTGC TATCTTGGTG GTCTCGGGCG TTGAC-
ATGCC ACCCCGACTA TGACGAAAAA CCATAGAAAC TAAGGAAGCA TGTTTTTT-
GG GACGACGGCA TCGTTGTGGC TCCATATCGT TCTTTCTGTA GATAAGCTGA GG-
CCCAGCGG CACGGGGTAG TTGGGGAGTA ATCCCAGTTC ACGTTACATC GGTTCT-
CTGG ACACGATTGC CCTGGCGACG ACAGCTCACA AACTCTGGCT TCAGAACGG-
G CTACTCCCTT CCGTAGTAAC TTACGTTCCC TCCGCGTGGG CGAGCCGAAT GAG-
TAGAATT TTCCCCGTAG ACAAAGCCTG TGAGCTGGCT TACAGTGACA GGCTTTC-
GCT ACTTGATGTA CGATTCTTTT AGGAGCCTCA GTTCGGAGAG TTAACTTAT CC-
CCTCGTA

8-11: CCTACTCC TGAACAACCA TCAGCGATAC TAATTGGCGT GTGTCTCG-
TA TGAACACCTG GCTCATCTAC CTCTTT GTTA GAACTATAAT AAGGTTCTGA A-
ATCTGTGTC TTACGCTCCT CGTCGCGGAT TAGGCCGGAG CAGAATCGGT CGAA-
TT CAGA TCATTTCGAT ATATGACGAG TCCTCCATGC TACAAAGAGC GCATGGG-
GCG AAAATACCCG ATAATACTTG GGCCAATATG GGCGCTGACT AAAAGTTGA-
G GTGGGACGCG CCCCTTGATA TAGCCCGACG CGGATAAAAT GCCTACCTAT C-
TC GCGAGCC TACATGCCCG TTTGGCGAAT TTAACGCCAT TTAAACTGAA AAAA-
CATAAC AGCCCCGGTG ACGGATGCTG GA ATCAAGGT AAATACGCAA TGCGAA-
CAGA TAGCCCTCAG CATGACCGCA GTGCGTACCC CCCGAGTCCA ATCCTGCTA-
T TTATCGCTCA GAGCACCGTC GTCGGCTAAC CACTCACTTG TCAAAATCGC AA-
CACCGATA TATCGTGCAA CCTATACTCA ATTCACACGG TCGTTCGCGG ACTCGC-
TGTT GCCGGATTGC GTGTGGGATG CATCGGGTAC TCAGGCTACG TAAGGACAG-
T GTTCTCCCTT TCGGACCGCT TTTAGAGACG CTACAGCGGT TTAGTTGGAA GCA-
CGGCCTC CGACTCCGGA CCCTTCTCAT AGGAAGGTGT TCTTTTACTT CTAGAACT-
GA ATAGGCAGCT TAAAATTTAG TTACAAGCAT TTCGGAAATG GCTACGTAAC A-
GCACAGGAC TTATACGGCG CGGTAGTCGG AAGTAACGCT TTGGTCAAGG CCCC-
ACAAAA GCAACCAAAC CAGAAAAC AG GACGAGATAA GTTTTTCCAT CGAATG-
TAAC GGAATGACCT TAGTTCGCTT AGGTGATGAT CGCACGAGTC TACGATAGT-
A TGGTGGGTAC CACGGCCGGC TACTCAGGCC CCGCACGGCG GAGTGGATGT C-
ATCAATGA CCCTCGTA

9-10: GGTCGAAA AAAAGTGTCG GCATCGTCCT AGCAAACAGG CCTACTCG-
TG TTTTACGTCC AAAGGAAACG CACT GGACAT AGAAAGTGCT CCTTTTACGA G-
ACATGCGTG TCTTCCCACG ATAGTCCCGC GGGAAGCTCA CGGAACTTAG GGTC-
TGTAAC AAATTCCGTA ACTCGGCTAC CCGAGGACAC GATTTACGAG GGGCGGT-
GGC CGGGGAAATA GCCCCACCAC GGCCGGGGAC CGGGTTAGTA CTCGTGGCG-
A GGGAAGGGCT CCAAAAGCCG TCGATCGCAC GATTCCGTCG GTCCGAGTCG C-
AGAAGGAGA CCAGACAGTC AGCGGCCGTA CCCAGAATGG CCAAAGCAAA GCC-
TAATTGC AGCACTGAAA GTAGCGGCGC GCCACCTGTT GGGGGATCTT ATTTCCT-
GTT GTCTGTCCTC GGAAATCAGA TTATGGAAAT CAGCATTATT CAAACACTTG C-
CTCAAGTGG ACACGGTGTA TCTCTCATCA TGACCGAAAA CGGGCTTTTA TACGT-
ACATG CATATCGCGT ACCCACATTT GACGTAGTAC TCGTCTTCAA TTCGTGGTT-
C GACTTGTAAG CCAGGCAGAG CCGCACCCTG GGTGTCAGTT TGCTGAAACT GG-
CCACTGCT AGCATATGCA CGAGCTTGTA TCTTCTCTCA ACCACCGGTG CCGCGG-
GGAG CAACGGGGA T CCTCGCTAAC TCAAGGCAAT TGCGGGGTGA GGGCCAGG-
CG TGACCTGGGT AGAGAACACA TTCACCAACA GAGCGCACAT CACATCATTA T-
ACTTGTTTG TACTTCTTAA AAAATTGCAC GGCGCTCCCT ACGTTAGTAT CTAGTC-
TTGA AATCTGTGGG CAGGCGGGGT GATCAACCGC TTCTAACGGA GCGAGATGC-
T AAAAGCATGA TTCACATTCT AGGGCAGGAA GGTATTGTTC ATAGAACTCC CT-
GGTCGTCG AGAAAAGATG TAACACTATC TGATCAAGCG ATGGATGAGC GATGG-
TATC ATT TGCCA.

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