Apply Acrydite™ Gel Separation to Solve Time-Table Problem

Zhixiang Yin¹, Min Chen²

¹School of Science, Anhui University of Science and Technology
Tianjiaan District, HuaiNan, Anhui province, China, ph:+8613855418993
²School of Science, Anhui University of Science and Technology
Tianjiaan District, Huai Nan, Anhui province, China, ph:+8613695545068
e-mail:zxyin66@163.com¹, chenmin0925@163.com²

Abstract

Time-table problem is a classical NP-complete problem. Algorithm of DNA computing for time-table problem was obtained with introducing the technology of Acrydite™ gel separation. Each class period viewed as a graph vertex was mapped into DNA molecules chain. With the probe coding, the gel column was constructed to arrange the order of DNA chain through biological reaction. The problem was solved by gel column that performs the basic core processing and extraction that makes the result visible. The minimum number of cycles of arrangement was the minimum number of class hours. The simulation results show that the algorithm compared with others is very easy and feasible.

Keywords: Time-table problem, Acrydite™ gel separation, DNA computing

Copyright © 2012 Universitas Ahmad Dahlan. All rights reserved.

1. Introduction

In 1962, C.C.Gotlieb presented a model for time-table problem on the article [1], which marks the time-table problem stepped into scientific field. In 1976, S.Even firstly proved the time-table problem is NP complete Problems in the article named [2]. Later on, in domestic, Linxi Zhang and Yaoru Lin working in Tsinghua University published their experimental research [3] about time-table problem in the Journal of Tsinghua University (natural version).In addition, some foreign scholars and domestic institutions of higher education [4-7] have been developed and employed with a quite good success one after another. More and more papers related to Time-Table problem have appeared in conferences and journals.

2. Acrydite™ Gel Separation

The basic idea of DNA computing model for time-table problem: the double helix structure of DNA and the Watson-Crick complementary condition are used to encode information, each class period viewed as a graph vertex is mapped into DNA molecules chain, create all kinds of data pool under the help of biological enzyme, and then according to some certain rules, original problem of data operation is highly parallel mapped into the controllable process with DNA molecules chains. The last step is to test the operation results by molecular biotechnology, such as PCR, ultrasonic degradation, clone, mutation, molecular purification, electrophoresis, magnetic bead separation. Although different models of DNA computing have their unique characteristics, they are all based on the molecular weight and the technology of electrophoretic separation with charge characteristics. Most of the models depend on the hybrid separation technology of Waston-Crick complementary condition. The precision of its calculation inquires its separation technology with the fast and accurate character, what’s important is that for some DNA Which content is little is also separated successfully.

Separation technology contains early gel separation, magnetic bead isolation technics, and the surface separation technology later provides a strong technical support for DNA computing involved separation requirements. Acrydite™ is a kind of chemical material which can connect modified as 5’end oligonucleotide based on acrylate and phosphorus amide. Acrydite molecular formula is C₁₉H₃₆N₃O₃P, its molecular weight is 385.48. Oligonucleotides controlled by Acrydite not only has covalent reaction with the surface controlled by mercaptan,
but also has the ability to combine each other to enter into polyacrylamide gel. Oligonucleotides controlled by Acrydite also makes macromolecule get the surface support through the covalent bonding of acrylic acid, which also can polymerize with acrylic monomer and has a reaction with sulfydryl and silicane[8-9].

Kenney[10] was the first man to find this technique in 1998, and then Braich[11] makes good use of the Acrydite™ gel separation to solve the 20 variables of the 3-SAT problem in 2002. The basic principle of the method about DNA computing is to use conventional DNA synthesis technology, HPAM is introduced to 5’end of oligonucleotide, the GGAT of HPAM is mixed with polyacrylamide to product gel layer with probes, and the way of gel separation is the standard method[12].

In this paper, DNA computing model for time-table problem is presented by using the technology of Acrydite™ gel separation.

3. Time-Table Problem

The time-table problem is a mathematical combinational optimization model of the problem of scheduling the school’s teaching program. According to some certain soft and hard conditions, the total scheduling contains human resource in teaching activity, material, time, space, and information is better used to meet a series of goals in time-table problem. We can see it as a problem that most events should be distributed in the limited time range. The reasonable and science arrangement of time-table will improve the activity of teachers and work enthusiasm, initiativ. It is directly related the image of school and its teaching order and quality of education. It is not only the schedule for teachers and students, but also has direct influence to other unified arrangement of school. It is one of the major issues to make the teaching management more scientization and modern by means of computer.

In short, each record about class coding, course coding, teacher coding and classroom coding and class hour coding can be viewed as a vertex. The first four codes have been known, only the class hour is left to determine. Any two vertexes have the same code of class, classroom, teacher in the graph are not allowed to arranged simultaneously, namely there is a correlation between the two vertex. Therefore, the time-table problem is solved by graph vertex coloring problem. So, the major problem we need to solve is to make the classes, classrooms, courses, and teachers distributed reasonably within a week.

The class hour is distributed as follows: each two lessons is seen as a time period for class, so there is five time period total a day (night lessons is one time period), then in one week, there is totally 25 time period, named finite set $T = \{T_1, T_2, \ldots, T_n\}$, as well, the classroom set is $C = \{c_1, c_2, \ldots, c_m\}$, teacher set is $X = \{x_1, x_2, \ldots, x_m\}$, class set is $Y = \{y_1, y_2, \ldots, y_n\}

A simple time-table problem is described as follows: there are $m$ teachers $(x_1, x_2, \ldots, x_m)$ and $n$ classes $(y_1, y_2, \ldots, y_n)$ in school. They are given a non-negative integer matrix $P = [p_{i,j}]$, called Requirements matrix, where $p_{i,j}$ is the number of classes given by teacher $x_i$ to class $y_j$. So, this article is to find the minimum time periods to arrange the time-table reasonable.

The course arrangement is recorded as matrix $P = [p_{i,j}]$:

$$
\begin{bmatrix}
x_1y_1 & x_2y_1 & \cdots & x_my_1 \\
x_1y_2 & x_2y_2 & \cdots & x_my_2 \\
\vdots & \vdots & \ddots & \vdots \\
x_1y_n & x_2y_n & \cdots & x_my_n
\end{bmatrix}
$$

If teacher $x_i$ gives a lesson to class $y_j$, then $x_1y_j = 1$, else $x_iy_j = 0$.

The article main purpose is to arrange the classes, classrooms, courses, teachers within a week and to confirm there is no conflict between them. The constraint conditions for time-table are as follows.
Accessorily matrices \( Q' = \{ q'_{ij} \} \) and \( Z' = \{ z'_{ij} \} \) are introduced. If class \( Y_i \) has a lesson in classroom \( C_j \) in time period \( t \), then \( q'_{ij} = 1 \), else \( q'_{ij} = 0 \). If teacher \( X_i \) are giving a lesson in the classroom \( C_j \) in time period \( t \), then \( z'_{ij} = 1 \), else \( z'_{ij} = 0 \).

The time-table problem is a problem to reasonably combine the classrooms, time periods, teachers and classes together in a certain constraint condition. If the solutions meet the hard constraints, they are feasible solutions, if they are still satisfied with the soft constraints, they are optimization solutions. So the ultimate aim is to seek out the optimization solutions to satisfy the need of the actual time-table problem. The constraint conditions in time-table problem are divided into hard constraint condition and soft constraint conditions.

The hard constraint conditions are that teachers and students are not allowed to meet the same event that is not in permission both in time and space. They are the basic constrained conditions.

(i) No class is allowed to be given by more than one teacher at the same period,

\[
q'_{ij} \times q'_{ij'} = 0, \quad i \in [1, n], \quad j \in [1, r], \quad t \in [1, 25] \tag{1}
\]

(ii) No teacher is allowed to give lessons in more than one classroom at the same period,

\[
z'_{ij} \times z'_{ij'} = 0, \quad i \in [1, n], \quad j \in [1, r], \quad t \in [1, 25] \tag{2}
\]

(iii) No classroom is allowed to be taken up by more than one class at the same period,

\[
q'_{ij} \times q'_{ij'} = 0, \quad i, i' \in [1, n], \quad i \neq i', \quad j \in [1, r], \quad t \in [1, 25] \tag{3}
\]

Soft constraint conditions are to make the time-table arrangement become more reasonable and homomization:

(i) The same course is spread out over a week, a teacher is not permitted to have lessons all day, the same course is not allowed to be given in the continuous time.

(ii) Try to satisfy some teacher’s special request.

(iii) It is better to arrange compulsory course in the morning, selective course in the afternoon, no lessons in the evening.

According to the fact, the premises are as follows:

(i) The capacities of the classrooms are never exceed.

(ii) Each course has its own particular teachers. For a class, the courses of this semester and their corresponding teachers have been told to teaching affairs office. So the information about the major course and teacher is viewed as a variable, noted as set \( s = \{ s_1, s_2, \ldots, s_n \} \) for all known information.

4. The DNA computing model for Time-table problem

Step1 The code of double-stranded DNA \( Y_j \) is constructed to represent the class, at the same time, its complementary strand \( Y_j \) is also constructed. Because there are \( n \) classes, it is necessary to contrast \( 2n \) double–stranded DNA, in addition, the DNA chain \( Y_j \) is fluorescence labeled.

Step2 Construct the gel column for DNA computing by putting DNA chain \( Y_j \) in order on condition that they are satisfied not only the hard and conditions but also the soft conditions.
Step 3: Adding the DNA chain $\overline{y}_j$, if the case happens that the double-chain area $\overline{y}_j$ is in the area of gel column, meaning the teacher $X_i$ is giving a lesson to class $Y_j$. Remove all gel column related to $X_i$ (the gel column about classes that the teacher $X_i$ needs to give is involved), let the remaining gel column for DNA computing continue to work.

Step 4: Repeat Step 3, in order to make each class conducts their own separate calculation, called a cycle, it is corresponding to a time-period.

Step 5: Until to get all $p_i$ for course arrangement, the number of cycles is the minimum time-periods that we need.

5. The Algorithm of Biological Implementation

Step 1: Create the pool of data. Create the double-stranded DNA $Y_1, Y_2, \ldots, Y_n$ to represent $n$ classes. At the same time, their complementary strand $\overline{Y}_1, \overline{Y}_2, \ldots, \overline{Y}_n$ are constructed and fluorescence labeled. Create the double-stranded DNA $C_1, C_2, \ldots, C_r$ to represent classrooms, in addition, their complementary strand $\overline{C}_1, \overline{C}_2, \ldots, \overline{C}_r$ are constructed and fluorescence labeled.

Supposing the teacher $X_i$ has to give lessons to $k_i$ classes, then $\sum_{i=1}^{n} k_i = n$.

Step 2: Create the gel column for DNA computing according to the constraint condition. The gel column is divided into $m$ parts, they respectively represent to teachers $X_1, X_2, \ldots, X_m$, each part is also divided into several layers, is determined by class the teacher needs to give lessons to and other constraint conditions. (For example, teacher $X_1$ needs to give lessons to classes $Y_1, Y_2, \ldots, Y_i$, so the $k_i$ layers are to combine to the area $X_1$. If teacher $X_1$ has to give a lesson to class $Y_j$ in the classroom $C_j$, the layer represents the classroom $C_j$ is in the area $X_1$ as the same. If the constraint condition is that both class $Y_j$ and class $Y_j'$ are having lessons in classroom $C_i$, the layer $C_i$ is under both the layer $Y_j$ and $Y_j'$). What needs to be stressed is that all area and layers can be addressed in operation.

Step 3: The step of gel electrophoresis is to add the DNA chains $\overline{y}_j$ and $\overline{c}_i$, what’s important is that sample volume of DNA chain $\overline{y}_j$ is less than the sample volume of DNA chain $Y_j'$, at the same time, the sample volume of DNA chain $\overline{c}_i$ is more than the sample of DNA chain $C_i$. According to Watson-Crick complementary principle, the DNA chains $\overline{y}_j$ and $Y_j'$ form double-stranded DNAs, which makes the DNA chain $\overline{y}_j$ fixed completely in the gel and captured by $Y_j$ ($Y_j > \overline{y}_j$), and has no ability to continue to move to the next area in the power of driving force under electrophoresis. Meanwhile, the DNA chain $\overline{c}_i$ is fixed completely in the area of gel $X_i$, and captured by $C_i$, the left chains are still moving in the power of driving force under electrophoresis, until all are captured by $C_i$ in the area of $X_i$. After finishing the first electrophoresis, the last step is to examine whether the captured DNA chains have a strong fluorescence response. Take $X_i Y_j, X_i C_j$ for example, if they are positive, so the conclusion is that the teacher $X_i$ is having a lesson to class $Y_j$ in the classroom $C_j$. Strip the area $X_i$ out.
from the gel column for DNA computing, the layer contained is included. The remaining gels continue to have electrophoresis.

Step 4 Repeat Step 3 until all are satisfied the constraint conditions.

Take \( P = \begin{bmatrix} 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 1 \\ 0 & 1 & 1 & 0 \end{bmatrix} \) for example, the hard condition:

(i) the two classes \( Y_i \) and \( Y_j \) only have their lessons in the classroom \( a \);

(ii) teacher \( X_1 \) gives lessons to class \( Y_j \) at the second time period;

(iii) If possible, the class \( Y_j \) has the priority to have a class compared with the class \( Y_{j+1} \). The diagram of gel column is shown in Figure 1.

\[
\begin{bmatrix}
Y_1 \\
Y_2 \\
Y_3 \\
Y_4
\end{bmatrix}
\]

\[
\begin{bmatrix}
X_1 \\
X_2 \\
X_3
\end{bmatrix}
\]

Figure 1. The diagram of gel column

6. The Discussion and Conclusion

The Acrydite technique usually employs the operation which is used the standard gel polymerization technique in current molecular biology laboratory widely to make DNA and gel crosslinked[13], highly active chemical crosslinking agent is not necessary in the process. The superficial density of hybrid probe of Acrydite technique to link DNA is up to 200 fmol, which is more favorable than the density of other connection methods. Although Acrydite\textsuperscript{TM} gel separation technique has been successfully applied in the area of DNA computing, it also has some shortcomings as follows. (1) Acrydite\textsuperscript{TM} gel separation technology as a means of separation technique takes too much time and human resource, it is unfavorable to solve the
large scale time-table problem. (2) In the model the biological automation degree is very low. It is inevitable for its limited gel length.

In the DNA computing model for time-table problem, two kinds of complementary code of DNA fragments will be hybridized and fixed on the capture layer if their corresponding class is having a lesson. The degree of automation is too low, and it’s inevitable for the limited gel length.

According to the condition of the classroom to design the gel electrophoresis column, add some complementary DNA chain by a certain order in the electrophoresis to guarantee that some class has the priority to have the same course.

Acknowledgments
The authors sincerely appreciate the encouraging comments of the Editor of the journal on this paper. They also wish to thank an anonymous referee of this paper who provided many useful and constructive suggestions for the improvement of this paper. Finally, thanks to all the authors that appear in the references. This paper supported by CNSF (Grant number: 60873144, 61170172,61073102,60973050).

References