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Design based on queue data structure and its implementation in DNA computer

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ABSTRACT

This paper analyzes the concept of queue, the storage structure of the queue data and encoding of the queue data based on queue data. After analyzing and giving an expression to the main structure of queue encoding, this paper discusses DNA encoding process of queue data through instance. Furthermore, an actual queue with details is given out to prove that it is feasible to encode queue structure data by DNA computer. The method and conclusion of this study may shed light upon other studies on the applications of DNA computer.

KEYWORDS

Queue data structure; DNA encoding; DNA computer.

INTRODUCTION

Molecular computing, whose core idea is to segment complicated problems deeply so that the methods to cope with complications can be more feasible, is an important part of contemporary computer computing. DNA computing is one actual method of molecular computing. In DNA computing, data waiting to be processed will be stored in DNA molecular, and then these stored data will be cut, hybridized and synthesized as the way of genetic engineering. This method can not only increase the data's storage density, but also ensure to highly parallel compute a great number of data, so it is wildly used in computer computing. DNA computer is a biological computer using DNA computing. It was invented from test tubes by Professor Leonard Adleman from University of Southern California. DNA computer can solve complicated math problems by operating in molecular biology way, which can apply deoxyribonucleic acid (DNA) to build up a complete information technology and take coding DNA sequences (generally known as computer memory) as operands. In the course of processing data in DNA computer, it needs to adopt different measures according to various structures. Queue data structure is the most common form in all data structures.

Researchers have carried out a lot of researches about DNA computer's queue data structure and had many key achievements. Lipton (1995) proved the operationality of solving satisfiability problems by DNA computing; on the basis of molecular computing connected subgraph, Ouyang (1997) explained the problem of maximal connected subgraph of queue data; Guar Nieri (1999) explored DNA computer to do add operation in the structure of rational number, and then concluded that queue data structure could reduce the difficulty of operation; after researching operation string and input string, Yurke (2002) found that both strings could be analyzed and encoded, furthermore, the form of encoded data structure was queue; Shapiro (2008) proposed that queue data structure could carry out automatic calculation at a finite state in DNA molecular, then constructed automata model. This model cut and circulated DNA molecular in the carrier of biological manipulated enzyme, and got the final state of queue data encoding as the form of exportable molecular; Shapiro (2010) did many specialized researches on controlling genes, so he believed that DNA computer could be used to control the expressing molecular of controlling genes. Through dissociating and constructing the queue data structure of expressing molecular, the shape of expressing molecular could be observed and estimated, so it would be much more targeted and visible for disease to be diagnosed.

DNA computer is different from a normal computer because it is more technical and specialized. Therefore, if DNA computer needs to be applied during solving some concrete problems, the data processed by it must be researched a lot to make complicated data become reasonable and simplified. To achieve this, it is necessary and feasible to apply a rational and convenient data structure for organizing efficiently the processed data of DNA computer. This research takes queue data structure as object. First, this paper analyzes and discusses the design methods and realizations of this type of data structure. Then, it carries out research on actual operations of queue data on DNA computer. It hopes that the ideas, methods and conclusions will supplement related researches and give some beneficial enlightenment to other related researchers.

THE CONCEPT, STORAGE STRUCTURE AND ENCODING OF QUEUE STRUCTURE IN DNA COMPUTER

The concept of queue

Linear list is the most basic, the simplest and the most widely used data structure. The data elements in the linear list are one-to-one relationships, meaning that all the data elements except the first one and the last one are linked end-to-end. Queue structure is a special linear list. In the queue structure, insertion of data can only be operated at the end of queue and data can only be eliminated at the front of queue. The insertion and elimination in the other positions are invalid. In the queue structure, data

processing strictly follows the sequencing, which means that the first in element (datum) in the queue quits first. Therefore, there are some scientists calling queue structure as first-in-first-out linear list. In the queue structure, there are pointers both at the front and end of queue, called as QueuePtr front and QueuePtr rear. Queue structure allows empty queue existing and computing. Under this situation, empty queue includes any element.

In DNA computer, queue can be stored according to the selectable structures. Generally, queue storage structure includes linked storage structure and sequential storage structure. In linked storage structure, the elements of queue will be separated into different logical types and stored as defined logical sequencing. Thus, linked storage structure has no requirement for the continuity of storage space and its stored data are stored by the logical lists. In sequential storage structure, storage space must be continued and in sequence and different sequential storage spaces store different logical data.

Encoding of the queue

Before processing data, first of all, DNA computer must transfer initial data into information recognized by computer program, the most critical of which is mapping the data, and this is the encoding of the queue. In this study, different methods of encoding present in different forms of combinations, and present as A, G, C, T in DNA area.

In the area of molecular biology, to achieve predetermined biochemical research results, one or several combined biochemical responses such as cut, hybridization, connection and synthesis usually are applied. These theories of biochemical response are also widely used in the area of DNA computer application. For these biochemical responses, because they have already had mature theories and applications in molecular biology, this paper will not discuss in details. In this study, queue is showed as the way of double-stranded DNA molecular. This study puts the encoding of the queue into the double-stranded DNA according to various logical sequences. Thus, queue will be stored into DNA computer as the way of sequential list. The storage space for DNA molecular is vast, so is the storage capacity. So, this study will not limit the length of queue or the overflow of the elements, nor discusses the possibility.

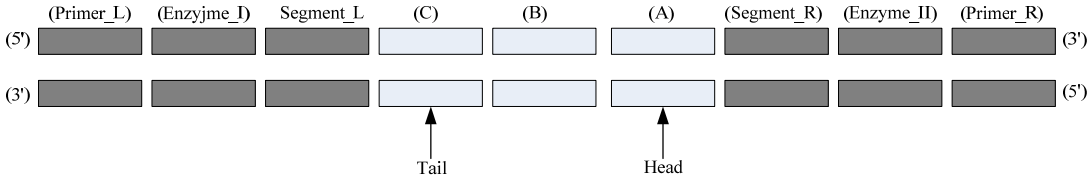

Figure 1 : Double-stranded DNA

Figure 1 shows that double-stranded DNA includes Primer-L, Enzyme-I, Segment-L, Segment-R, Enzyme-II, Primer-R and queue elements. Among these parts:

(1) Enzyme-I is a recognition site. It can cut DNA strand under the condition of restriction enzyme being active. It's worth noting that the cut must process at the rear of queue structure. The cut section is used to be connected or hybridized with the elements waiting for entering in the queue, and it puts those waiting elements into the queue structure under the role of ligase.

(2) Enzyme-II is similar to Enzyme-I, which is also a recognition site. When this kind of restriction enzyme is activated, the pending queue for processing will be cut. What is different from Enzyme-I is that Enzyme-II's cut operation happens at the front of the queue. In this research, detector is a pre-designed fragment. Ligase will connect and hybridize the detector and the fragment cut by enzyme in Enzyme-II. The newly formed fragment is ready to do dequeue operations. Detector will record the value of elements out of the queue. So when the researchers have difficulty to obtain the information of dequeue elements, they can get them through detector much easier.

It's worth noting that though Enzyme-II has the same processing procedure for data elements as Enzyme-I, the restriction enzymes they employ are not the same. Otherwise, the elements they processed would bring the same character so that the dequeue program could not finish.

(3) Segment-L and Segment-R contain base pairs equipped with certain character. When double-stranded DNA is on the enqueue or dequeue operations, the base pairs contained in Segment-L and Segment-R will finish the cut operation activated by enzyme to the double-stranded DNA at the proposed point on the basis of its own length.

(4) As primers, Primer-L and Primer-R are set in both ends of the double-stranded structure. They are designed in advance to be used to trigger PCR reaction. The density of reactants must be ensured in order to ensure the efficiency and effect of the biochemical reactions. During DNA computing, to ensure that there is enough DNA strands, PCR reaction is used to amplify the strands.

The common operations of the queue

The common operations of the queue in DNA computer include the enqueue of elements, initiation of queue and the dequeue of elements. This paper will discuss these common operations as followings. The letter Q represents a queue.

(1) The initiation of Q queue: Bio-Initiate(Q)

Empty queue is the queue without any element. As Figure 2 showing, empty queue contains other DNA strands' elements except elements. In order to the convenience of computer operation, the study indicates the initiation of empty queue as Bio-Intiate(Q). Figure 3 shows that the realization of the initiation of the queue needs its antisense strand. Therefore, firstly, DNA encoding needs to split into two strands, either of which is the normal strand Q1 and the antisense strand A1. It's worth noting that A1 and Q1 are two complementary strands. Next, A1 and Q1 have to receive the annealing response at appropriate temperature environment. Finally, double-stranded DNA is formed and it is the empty queue needed in the research.

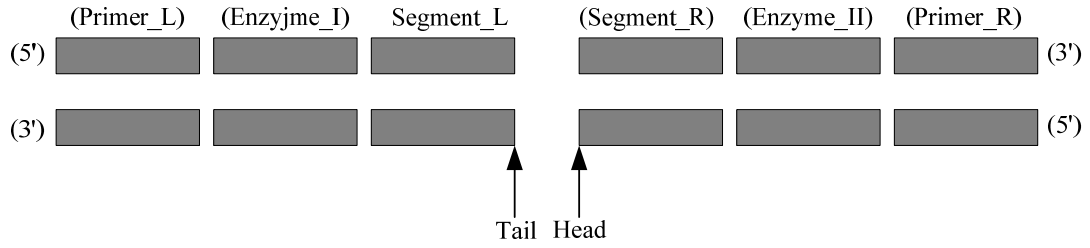

Figure 2 : The structure of empty queue

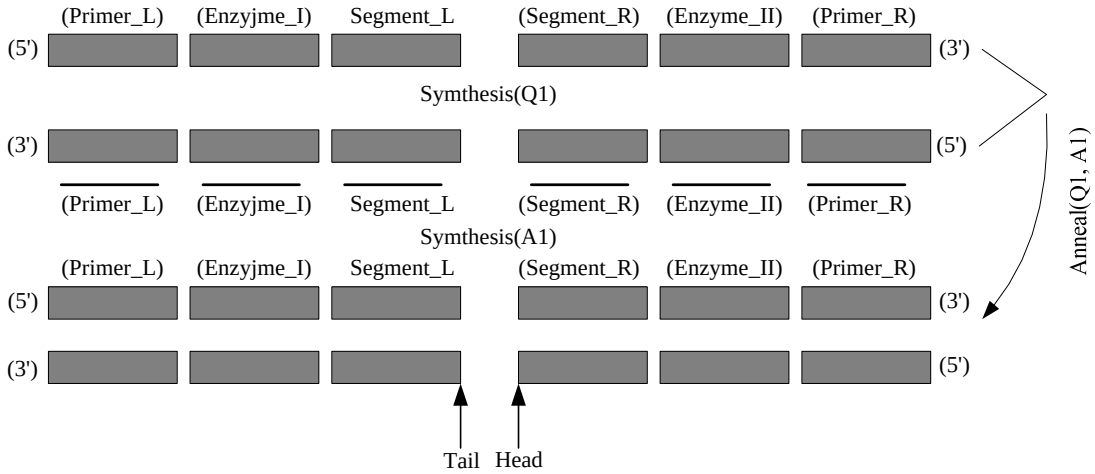

Figure 3 : The procedure of Bio-Initiate(Q)

(2) The enqueue of elements: Bio-Enter (Q,X)

The operation of the enqueue of elements must finish at the rear of queue. For the convenience of computer processing, the study indicates Bio-Enter (Q,X) as the enqueue of elements. Figure 4 shows that there are three procedures of the enqueue of elements. In this process, the location of X at the rear of the queue will be recorded by detector. At the same time, restriction enzyme Enzyme-I shall be activated, which will cut double-stranded DNA molecular on the location of X. The newly formed fragment will be separated as left and right, either of which contains one single cohesive end. Meanwhile, ligase at the rear of the queue will connect and hybridize both newly formed fragments. In the end, the intact double-stranded DNA is formed and X is put into the rear of the queue. Thanks to the identification point of restriction enzyme (Enzyme-I) having been put in the encoding of X, the enqueue operations after this will go on smoothly.

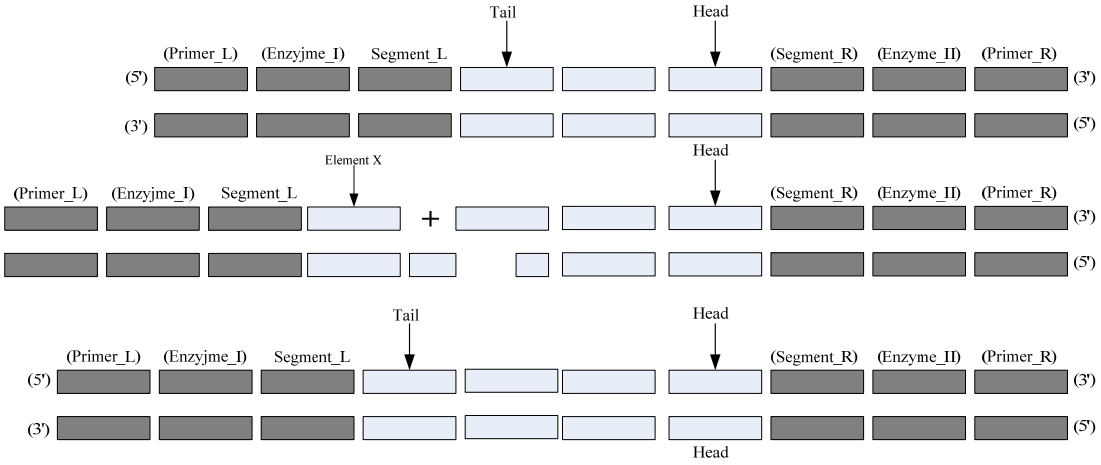

Figure 4 : The process of Bio-Enter (Q,X)

(3) The dequeue of elements: Bio-Get out (Q,X)

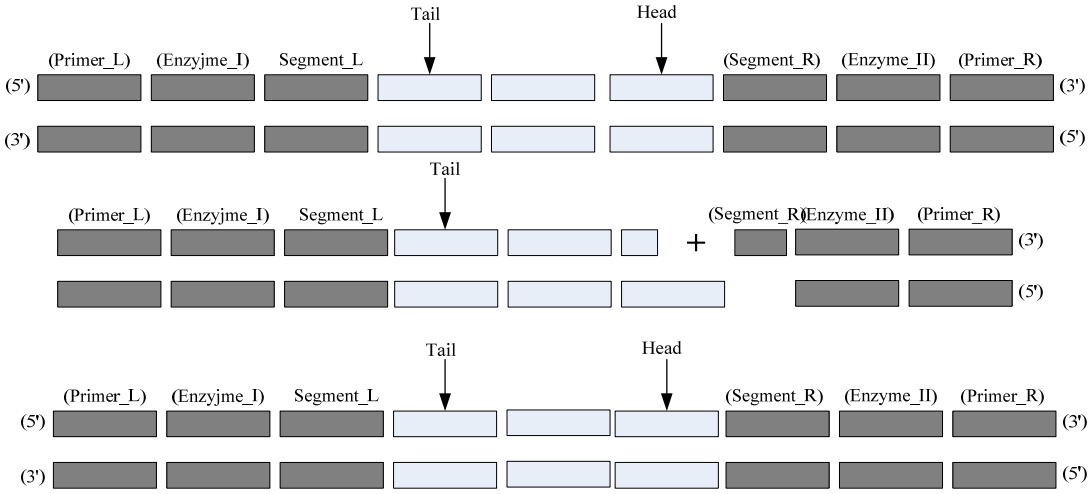

Figure 5 : The process of Bio-Get out (Q,X)

The dequeue of elements means that the elements at the front through processing to be obtained value and eliminated from the queue. For the convenience of computer processing, the study indicates the dequeue of elements as Bio-Get out (Q,X). The procedure of the dequeue of elements shows as Figure 5. The object of dequeue is the elements at the front of the queue. The front elements get out the queue only if the restriction enzyme is active, so Enzyme-II is activated. At the front of the queue, detector fragments have recorded the location of Q queue where double-stranded DNA is cut. Then, left and right new fragments are formed. Both of them have one cohesive end and two ends are complementary strongly. Prepared detector fragment also has a cohesive end which is complementary strongly with the cohesive end of the newly formed left fragment. So detector will connect and hybridize with left fragment under the effect of ligase and form new DNA molecular, which represents a new queue structure. Besides, in order to obtain the value of elements of the queue easily, DNA computing program designs a unique detector for each element of the queue. The unique detector has complementary cohesive ends with the left fragments. If the final connected DNA molecular is detector-empty molecular (which is specialized marked the state of empty element), it is for sure that the current processing queue is empty and the dequeue of elements is done.

INSTANCE OF ARITHMETIC OF QUEUE STRUCTURE

Through above discussion, the study will give an example to explain how to realize the arithmetic of queue in DNA computer. In the instance, A, B and C are three queue elements and the DNA encoding of the queue which A, B and C belong to has already been given.

DNA encoding of the queue

In the instance given by this study, Fok1 is the restriction enzyme at the rear of the queue (Enzyme-I). Its cut point is (9,13) and recognition site is 5c-GGATG-3c. Accordingly, BsmFI is the restriction enzyme at the front of the queue (Enzyme-II). Its cut point is (10,14) and recognition site is 5c-GGGAC-3c. From Figure 6(a) to Figure 6(c), the numbers in the box of DNA encoding represents basic groups, which are ambiguous and uncertain. These basic groups are the elements forming DNA in the instance. It is worth noting that this DNA only has 5c-GGATG-3c and 5c-GGGAC-3c recognition sites by enzyme. DNA encoding of Figure 6(a) belongs to Q queue. It can be seen that Q queue includes three elements, A, B and C, and each of whose DNA encoding is in Figure 6(b). From Figure 6(b), it can be found that the encoding of A, B, C has its own recognition site 5c-GGATG-3c recognized by restriction enzyme FokI. Moreover, their cohesive ends are the same so that it is ensured the correctness of subsequent enqueue operation. The encoding showed in Figure 6(b) is set up four different basic groups on the left near the cohesive ends in order to distinguish A, B and C. Different queue elements correspond to different detector molecular.

Instance of arithmetic

Figure 7 shows the simple arithmetic of the queue of 3.1 in DNA computer.

```
Algorithm // ** Queue Q is empty when staring ** //
 {Bio-Initiate (Q);
  Bio-Enter(Q,A);
  Bio-Enter(Q,B);
  Bio-Getout(Q,X);
  Bio-Enter(Q,C);
 }
```

Figure 7 : Instance of arithmetic based on Q queue

CONCLUSION

The study not only discusses the concept of queue, the storage structure and methods of encoding, but also verifies the implementation of computing queue structure in DNA computer and illustrates by an instance. The arithmetic shows the correctness of this paper's inferences and argumentations. The results of this research can assist further studies of DNA computer and related topics.

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