Chapter 5
DNA Computing

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ABSTRACT

DNA computing is widely accepted as a new computing framework all over the world. In this chapter, the background of DNA computing is firstly introduced by solving a Hamilton Path problem. Then three research directions are proposed according to the current development of it, including the theoretical framework, practical DNA computing models and DNA encoding. In each part of the three research directions, many recent results are involved. In the theoretical framework, DNA computing is proved to be computationally universal by four formal DNA computing models. In practical DNA computing models, DNA computing is shown to solve NP-complete problems and work well in other fields, such as medical science. In DNA encoding, some DNA codes and encoding methods are introduced to avoid the false positive phenomenon. And they have a final purpose in common: constructing a universal Biomolecular computing model, which is also called as biomolecular computer, to solve intractable problems for electrical computers. Finally, some further research directions are shown in each part for the design of biomolecular computer.

1. INTRODUCTION

Biomolecular computing, especially DNA computing, is a biologically inspired computing method. Biomolecular and bio-chemistry operations are introduced in solving hard problems in DNA computing. So it is quite a great advancement of soft computing in the 20th century and it also plays an important role in constructing low energy costing and huge information storing computing models. Nowadays it has been widely accepted as a new computing model for future computing devices in computer science. As we know, NP-
hard and NP-complete problems are intractable to be solved in polynomial time by electrical computers when the size of problems becomes large. DNA computing was firstly proposed to solve these computationally hard problems by biological models. It is novel to solve problems by taking DNA molecules as computing paradigms and bio-chemistry operations as tools in realistic world. More and more computationally hard problems are considered to be solved by this novel computing device. The hugely storing information ability, parallel computing ability and lower computing energy cost make DNA computing to be a perfect computing paradigm. DNA computer based on DNA computing earn much attention all over the world.

In this chapter, DNA computing is mainly discussed as a new computing method. In section 2, the birth and development of DNA computing are introduced. Three research aspects of DNA computing and their relationship are introduced in detail in this section too. The theoretical framework of DNA computing, including formal DNA computing models and theoretical DNA computing models, are discussed in section 3. Three main formal DNA computing models are proved to be computational universal and their computing complexities are considered. In section 4, some DNA computing models which are used to solve realistic problems, such as Benenson Automata, are introduced. DNA encoding, including DNA encoding metrics and methods, are involved in section 5. Finally, some further researching directions are discussed in section 6.

2. THE BIRTH AND DEVELOPMENT OF DNA COMPUTING

DNA computing, firstly proposed to solve HPP with seven vertexes, is quite a new method in solving NP-complete problems. DNA computing is proved to be much more effective in solving NP-complete problems. Since then it has attracted important attention from scientific community with contributions to mathematics, biology, chemistry and computer science, enriching each other with results, opening problems and promising new research lines. The eventual purpose of DNA computing is to design DNA computers, also called biological computers, which are universal computing devices and much more powerful than electrical computers. There are three main research aspects in DNA computing: theoretical framework of DNA computing, DNA computing models in practice and DNA encoding. The above three researching aspects together contribute to the invention of DNA computer.

**Adleman’s DNA Computing Algorithm**

In 1994, Adleman [Adleman94] firstly proposed DNA computing algorithm, by which a Hamilton Path Problem (HPP) with 7 vertexes is solved only using DNA molecular and biochemistry operations. Three steps were mainly introduced in Adelman’s algorithm: encoding all paths, deleting unsatisfactory paths and reading out satisfactory paths. The involved bio-chemistry operations include hybridization, melting, filtrating, PCR amplification, probe detecting, DNA sequencing technology, etc. The HPP solved by Adleman is shown in Figure 1 and the flowchart of Adleman’s algorithm in Figure 2.

In Adleman’s algorithm, each vertex is encoded into 20-bases DNA strand randomly. Then all the seven DNA strands are put into an initial tube labeled tube1. Since there are thirteen edges in Figure 1, thirteen 20-bases long edge single DNA molecules are designed according to the molecules encoding the seven vertexes and added into the tube1. Now tube1 is known as the initial solutions space of the HPP. According to the Watson-Crick principle(A&T bonded and G&C bonded), single DNA molecules can hybridize to double DNA molecules in a very short time.
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