The Application of DNA Self-Assembly Model for Bin Packing Problem

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ABSTRACT

Bin Packing Problem (BPP) is a classical combinatorial optimization problem of graph theory, which has been proved to be NP-complete, and has high computational complexity. DNA self-assembly, a formal model of crystal growth, has been proposed as a mechanism for the bottom-up fabrication of autonomous DNA computing. In this paper, the authors propose a DNA self-assembly model for solving the BPP, this model consists of two units: grouping based on binary method and subtraction system. The great advantage of the model is that the number of DNA tile types used in the model is constant and it can solve any BPP within linear time. This work demonstrates the ability of DNA tiles to solve other NP-complete problems in the future.

Keywords: Bin Packing Problem, DNA Computing, DNA Tile, Self-Assembly, Tile Assembly Model

INTRODUCTION

The BPP can be simply described as follows: put a certain number of items into some boxes with the same volume, make the volume sum of the items in each box not exceed the volume of the box, and finally ensure that the number of the boxes used in the process is the least. It is a typical combinatorial optimization problem, and involved in many fields, especially in the field of computer science and industry, it has extensive application background, such as multi-processor scheduling, memory management, resource allocation, transportation plan and so on (Johnson, 1974), so the research of bin packing problem has wide application value.

Up to now, researchers have proposed many solutions and approximation algorithms to solve the BPP, such as the grouping genetic algorithm (Falkenauer, 1996), hybrid genetic algorithm (Reeves, 1996), Ant colony optimization (Levine & Ducatelle, 2004),...
the next adaptation, the first adaptation, the descending next fit, the best adaptation and so on (Coffman, Garey, & Johnson, 1996), whereas the results have a great relationship with the volume of the items when using these approximate algorithm to solve the problem with complex constraints.

However, the DNA self-assembly can solve the above problem in theory. DNA self-assembly is one of the most important applications of DNA computation, and the process is cost effective, versatile, facile, and the process occurs towards the system’s thermodynamic minima, resulting in stable and robust structures (Lehn, 1993). The relation of DNA computation with self-assembling structures was developed in the mid-1990s, largely through the theoretical and experimental work of Adleman (1994), Winfree, Eng, and Rozenberg (2001) Winfree (1998), Seeman (1998), Reif (2002), and Rozenberg and Spaink (2003). Because of its massive parallel computing function and large amounts of information storage ability, it has gradually become a mainstream method to solve the basic arithmetic problems and NP-Complete problems. For example, Arithmetic computation in the tile assembly model: Addition and multiplication (Brun, 2007), Arithmetic computation using self-assembly of DNA tiles: subtraction and division (Brun, 2008), Solving satisfiability in the tile assembly model with a constant-size tileset (Zhang, Wang, Chen, Xu, & Cui, 2009), DNA self-assembly for the minimum vertex cover problem (Wang, Hu, Zhang, & Cui, 2011), DNA 3D self-assembly algorithmic model to solve the maximum clique problem (Ma, Li, & Dong, 2011), 3D DNA self-assembly model for graph vertex coloring (Lin, Xu, & Zhang, 2010), Application of DNA computing by self-assembly on 0-1 knapsack problem (Cui, Li, Zhang, Wang, Qi, Li, & Li, 2009), Application of DNA self-assembly on maximum clique problem (Cui, Li, Li, Zhang, & Li, 2009), DNA tile assembly model for 0-1 knapsack problem (Wang, Lu, Zhang, & Cui, 2010) and so on.

In this paper, we propose a DNA self-assembly model with a subtraction system for solving the Bin Packing problem. The rest of the paper is organized as follows: First we describe the basic knowledge and the mechanism of DNA self-assembly; we give the definition of the Bin Packing problem; we then show the DNA self-assembly model for solving the Bin Packing problem; finally, we give a conclusion.

DNA TILE ASSEMBLY MODEL

The tile assembly model is a formal model of crystal growth. It was designed to imitate molecules self-assembly such as DNA. It is a partial extension of a model proposed by Wang (1961). The model was fully defined by Rothemund and Winfree (2000), the model has tiles that stick or do not stick together based on the binding domains on their four sides. Each tile has a binding domain on its east, west, south and north side, and may bind with another tile when the binding domains on the adjoining sides of those tiles match and the total strength of all the binding domains on that tile exceeds the current temperature. The type of the tile is defined according to the four binding domains. In this definition, the tiles are not allowed to rotate. I will restate some useful definitions here to assist the reader. Abstract Tile assembly model mainly consists of four parts:

1. **Basic Tile**: It can be used as any kind of calculating operator, and stores operation values, it is the basic unit of DNA self-assembly calculation. The edges of it can represent different calculation operators or numerical values;
2. **Framework Tile or Seed Configuration**: Used to construct the start and end of assembly of a self-assembly body;
3. **Function of bonding strength g**: For defining the bonding strength between any two edges of Tile;
4. **Parameter τ**: A parameter to judge whether the combination of tiles is stable, only when the sum of the bonding strength between tiles is larger than τ, the assembly body can achieve stability.
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