

# A Molecular Solution to the Three-Partition Problem

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## ABSTRACT

*Given a set of numbers, the three - partition problem is to divide them into disjoint triplets that all have the same sum. The problem is NP - complete. This paper presents an algorithm to solve this problem using the biomolecular computing approach. The algorithm uses a distinctive encoding technique that depends on the numbers values which omits the need to an adder to find the sum. The algorithm is explained and an analysis of its complexity in terms of time, the number of strands, number of tubes, and the longest library strand used is presented. A simulation of the algorithm is implemented and tested. This algorithm further proves the ability of molecular computing in solving hard problems.*

*Keywords: Complexity, DNA Computing, DNA Encoding, Molecular Computing, Natural Computing, Simulation, Three-Partition Problem*

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## INTRODUCTION

DNA, or deoxyribonucleic acid, is the material that carries information across generations. Rather than storing information in binary form as in digital computers, the information in DNA is stored as a code made up of four chemical bases: adenine (A), guanine (G), cytosine (C), and thymine (T). DNA bases pair up with each other to form units that are called base pairs such that A binds with T and C binds with G. This is known as Watson-Crick complementarity.

Each DNA base (deoxyribonucleotide) consists of three components: a sugar, a phosphate group, and a nitrogenous base. A DNA strand has two different ends that determine its polarity: the 3' end, and the 5' end.

A DNA sequence (strand) of length  $n$  consists of  $n$  consecutive letters from the set  $\{A,$

$G, C, T\}$ , which is similar in computer science to a string consisting of a combination of four different symbols A G C T.

Thousands of biological databases that store DNA sequences exist and some of the well known databases are the Genbank that has a collection of all publicly available DNA sequences (<http://www.ncbi.nlm.nih.gov/genbank/>), and The Reference Sequence (RefSeq) collection which aims to provide a comprehensive, integrated, non-redundant, well-annotated set of sequences, including genomic DNA, transcripts, and proteins (<http://www.ncbi.nlm.nih.gov/RefSeq/>). Biological databases should provide biologists with central and uniform access to their data. Several methods exist to deal with providing users with accurate data efficiently regardless of the heterogeneity of database (Singh, 2003; Wang et. al., 2009).

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The specificities of nanotechnology data and applications suggest implementing an ad-hoc tool that allows updating information frequently, so that not only the latest versions of the documents are always available, but also the raw experimental data are shared in a protected environment (Giacomini et al., 2009). These huge data are critical for both biologists, to understand how natural systems work, and other scientists to use these data to solve other computational problems.

Molecular computing, also known as DNA computing or natural computing, is a new approach to parallel computation where computing takes place in test tubes; it uses DNA, biochemistry and molecular biology, instead of the traditional silicon-based computers. Using this approach, several NP-complete problems were solved with a polynomial number of steps (Adleman, 1994; Brun, 2008; Chang et al., 2004; Chang, 2007). The theory behind the solution is based on representing problem instances with DNA sequences. Now, you can order DNA sequences and receive them within few days. After receiving these sequences, several molecular operations are applied in a specific order on these sequences. The resulting DNA sequences (if any) usually specify the problem's correct solution.

DNA computing has been applied to different problems that range from very simple computations such as adding two numbers (Wasiewicz et al., 2000; Gupta et al., 1997) to very complex problems such as intractable problems (Tanaka et al., 2005). Although simple computations took much more time using DNAC than silicon-based computers, they showed the ability of DNA computers to mimic traditional computers.

Moreover, various fields of study used DNA computation. This includes computer science (Kim et al., 2008), mathematics (Shi & Chu, 2010), Engineering (Nuser, 2010) . . . and others. The main benefit of using DNAC in these fields is that always all possible solutions are created and processed simultaneously offering a huge parallelism that solves problems efficiently.

An advantage that silicon based computers has over DNA computers is the extreme speed of solving simple problems such as adding two numbers. This leads to a question of what applications are suitable to be solved with DNA computers. This is an open question that is not solved yet, but most DNAC researches lead us to increase the possibility of the suitability of medium sized NP-complete problem instances to be solved by DNA. This is because the time to solve these kinds of problems grows exponentially with the problem size. Therefore, silicon-based computers can solve the problem efficiently until a specific size at which DNA computers work more efficiently than silicon-based computers. When problem instances become very large both types of computers become incapable.

Traditional silicon-based computers have several limitations such as: circuit integration dimensions, clock frequency, power consumption and heat dissipation (Saravanan, 2009).

Molecular computer offers much lower power consumption than traditional silicon-based computer. It has a huge capacity storing data in a trillion times less space than traditional computers. In addition, it has an enormous parallelism where trillions of DNA molecules perform computations simultaneously (Adleman, 1994).

The following sections will discuss a literature review of DNA computing, followed by several applications of DNAC, and then a number of approaches in DNA computing will be discussed.

Details of the molecular computing and its operations will be discussed, followed by computer simulation of *in vitro* operations.

The three-partition problem will be explained next. A computer based algorithm to solve the problem will be shown followed by a molecular computing algorithm. A simulation of the solution to an instance of the three partition problem will be demonstrated, and then a conclusion and future work will be shown.

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