Chapter III

DNA Computing and Errors: A Computer Science Perspective

Lila Kari, The University of Western Ontario, Canada

Elena Losseva, The University of Western Ontario, Canada

Petr Sosík,
Silesian University, Czech Republic and
The University of Western Ontario, Canada

ABSTRACT

This chapter looks at the question of managing errors that arise in DNA-based computation. Due to the inaccuracy of biochemical reactions, the experimental implementation of a DNA computation may lead to incorrectly calculated results. This chapter explores different methods that can assist in the reduction of such occurrences. The solutions to the problem of erroneous biocomputations are presented from the perspective of computer science techniques. Three main aspects of dealing with errors are covered: software simulations, algorithmic approaches, and theoretical methods. The objective of this survey is to explain how these tools can reduce errors associated with DNA computing.
INTRODUCTION

Biomolecular computing is a field that studies biologically based computational paradigms that serve as alternatives to the traditional electronic ones. Biomolecular computing includes DNA computing (Adleman, 1994; Head, 1987), RNA computing (Faulhammer et al., 2000), peptide computing (Balan et al., 2002), and membrane computing (Păun, 2000). The main idea behind DNA computing is that data can be encoded in DNA strands and molecular biology tools can be used to perform arithmetic and logic operations.

Nearly a decade has passed since the field of DNA computing premiered on the scientific stage as the possible computational paradigm of the future. The idea attracted research from a wide spectrum of mathematical and natural sciences. However, the inherently complex nature of biological processes tempered the advancement of the field, suggesting the development of biocomputing will trail a path that is different from that of electronic computing half a century ago. It is becoming increasingly more apparent that most plausible implementations of biocomputing are likely to produce some unexpected and erroneous results. From chemical reactions in vitro that occasionally have unpredicted output, to unforeseen problems in vivo, it seems that many errors are not only inevitable but also an integral part of the biological processes. The purpose of this chapter is to provide a survey of the tools that computer scientists offer for dealing with the imminent problem of managing errors in DNA computing.

The battle for reliability of biomolecular computation and reduction of errors can be fought on several fronts. Research is conducted to find better ways to encode information in DNA, to develop more efficient algorithms, and to improve laboratory techniques, among other results. This survey does not cover the wide scope of research in chemistry, biology, physics, or engineering that contributes to dealing with errors in biomolecular computing. Instead, this exposition explores the tools that computer science offers us in managing the errors that arise in DNA computing processes.

A single strand of DNA (deoxyribonucleic acid) is a molecule made of a sequence of nucleotides, also called bases. Four types of nucleotides are present in DNA, called adenine, guanine, cytosine, and thymine. These are abbreviated as A, G, C, and T respectively. A single strand of DNA is held together by covalent bonds that keep the bases linearly attached to each other. In addition, it is possible for hydrogen bonds to form between the A and T bases, as well as between C and G bases of two different strands. This property is referred to as the complementarity of nucleotides — that is, A and T are said to be complementary, and so are the C and G bases. Bonds between
Full Adder Operation Based on Si Nanodot Array Device with Multiple Inputs and Outputs
www.igi-global.com/article/full-adder-operation-based-nanodot/4078?camid=4v1a